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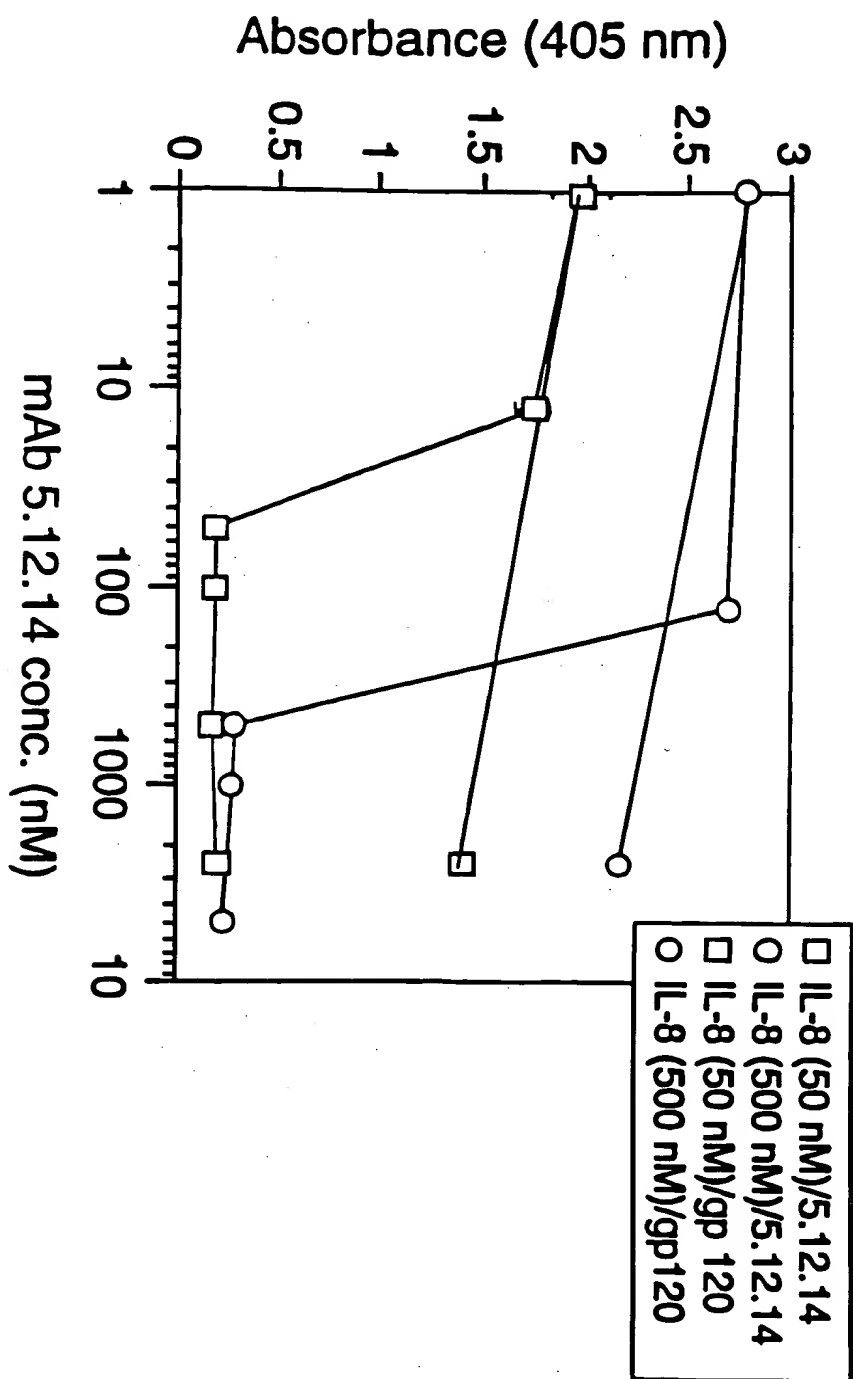
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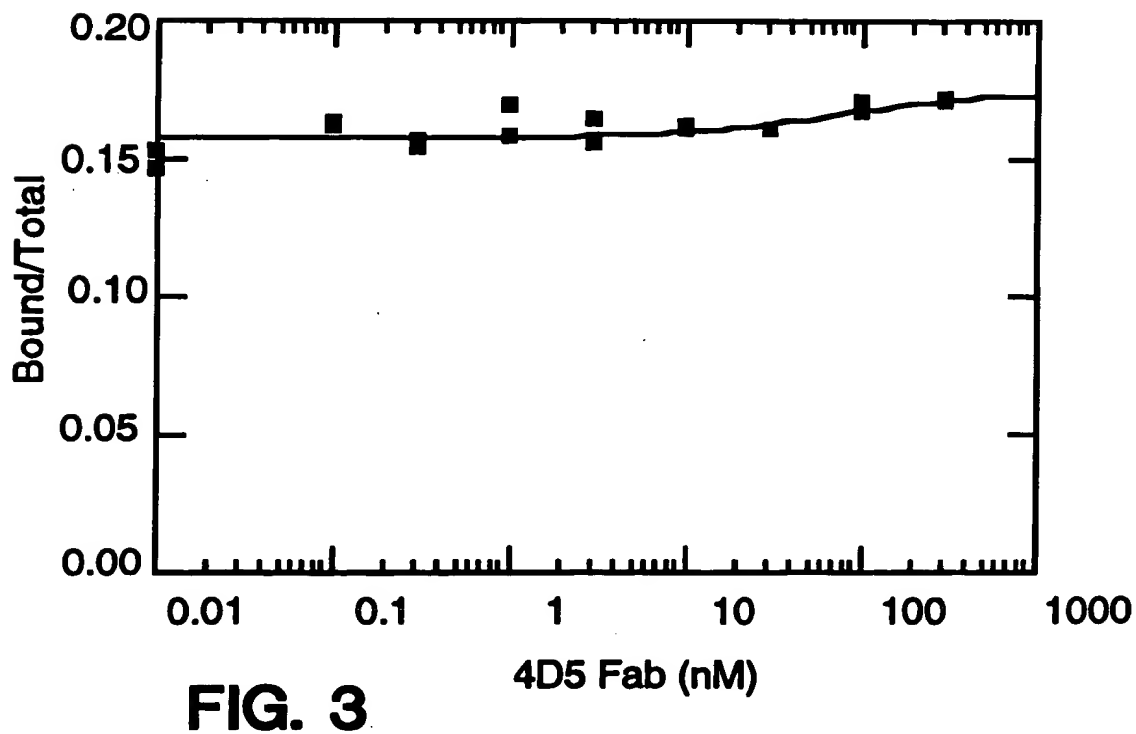
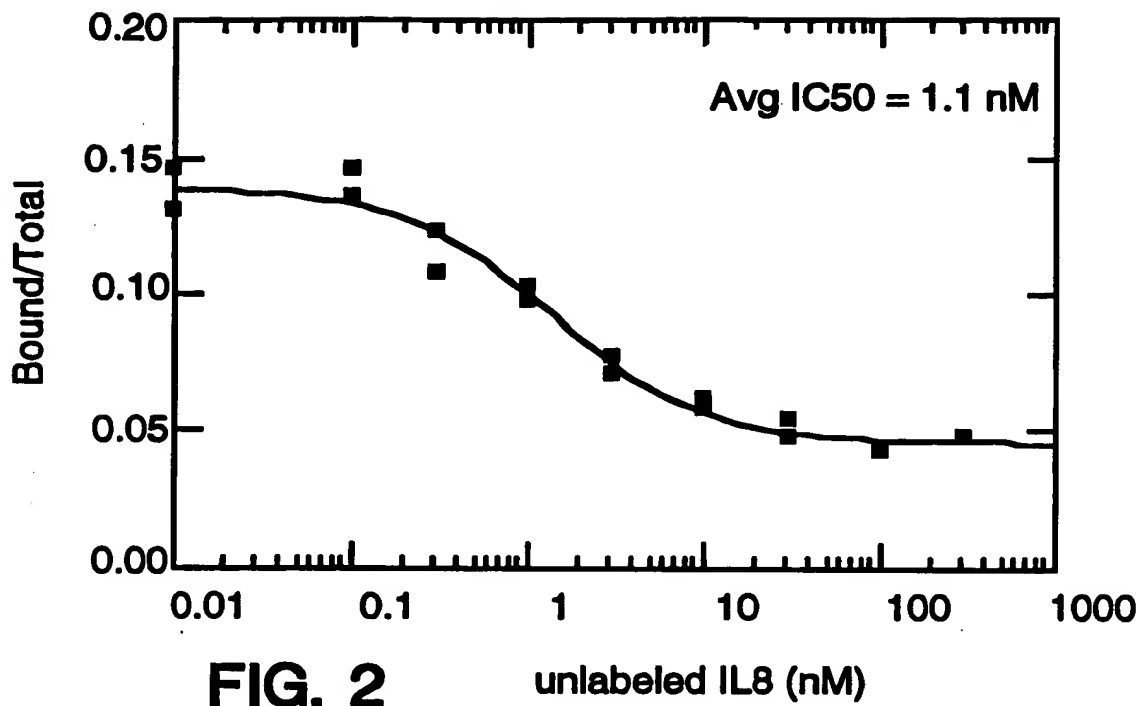
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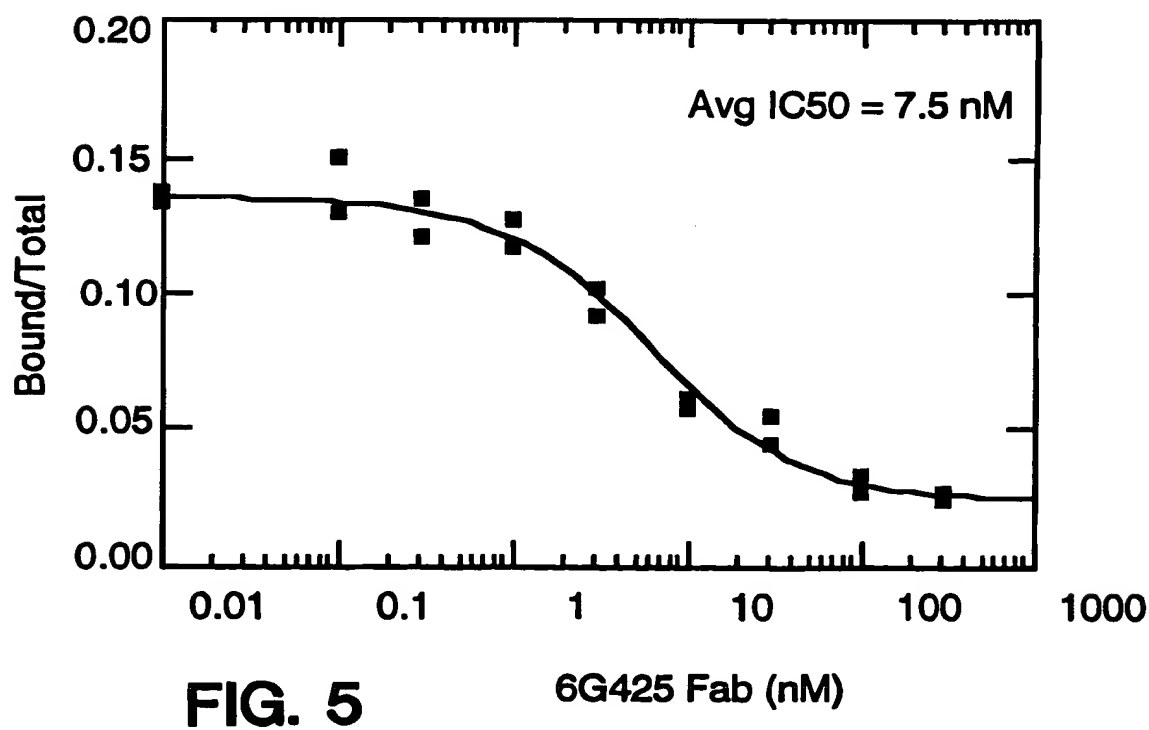
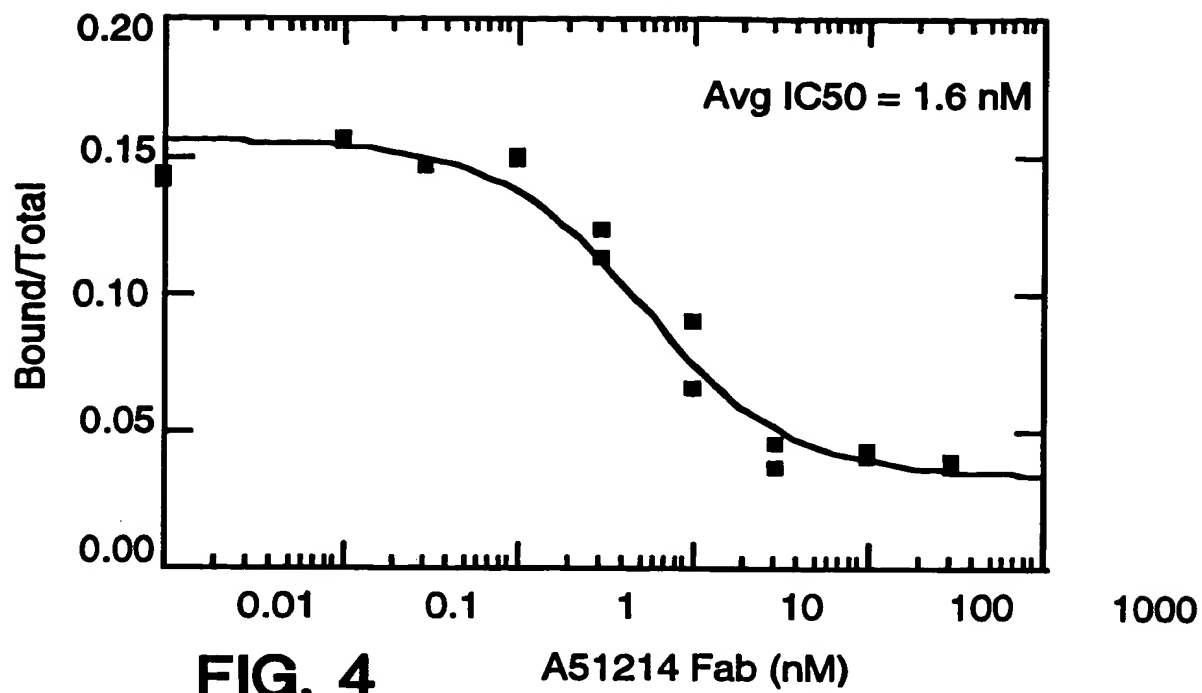
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FIG. 1







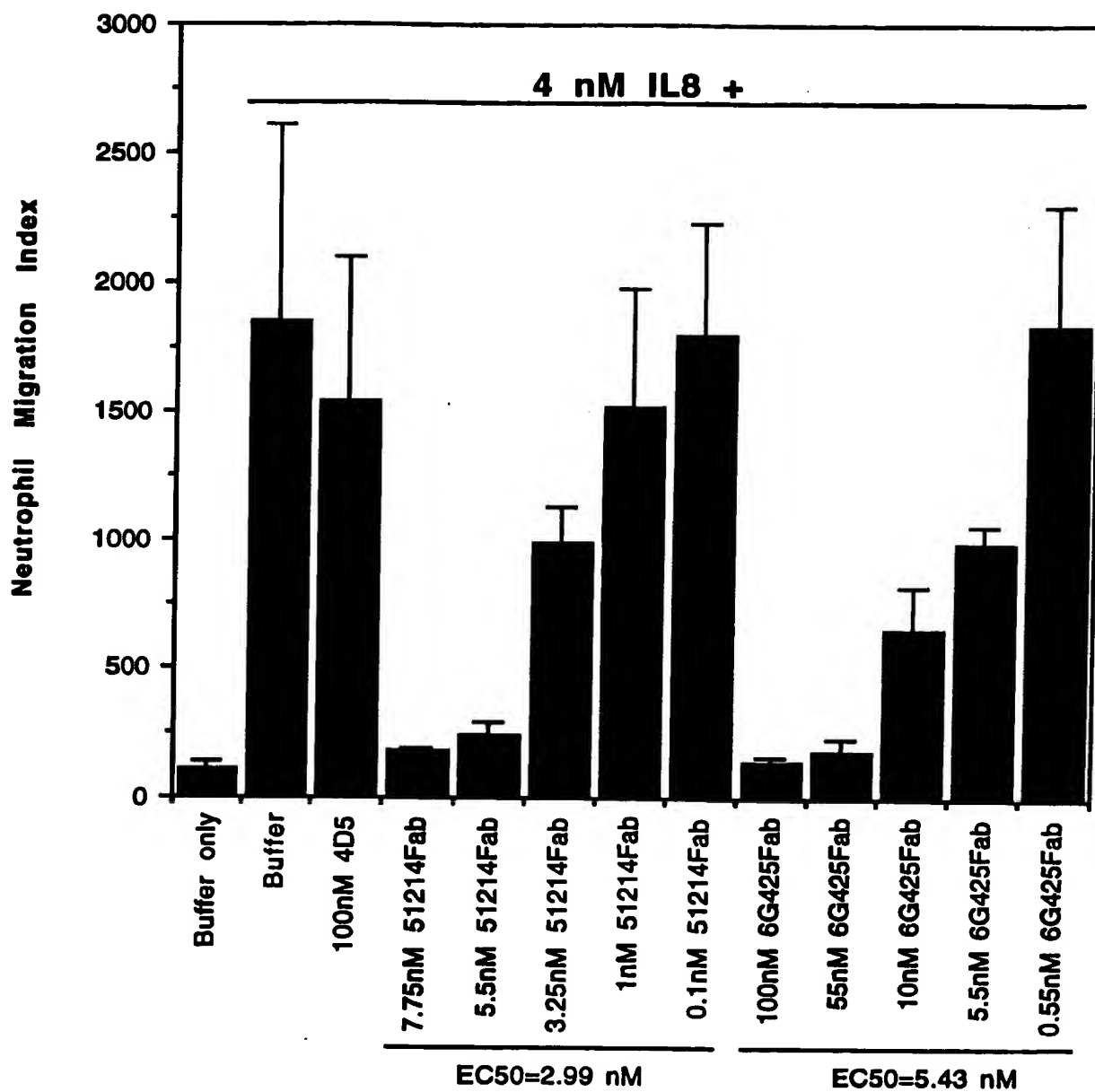


FIG. 6

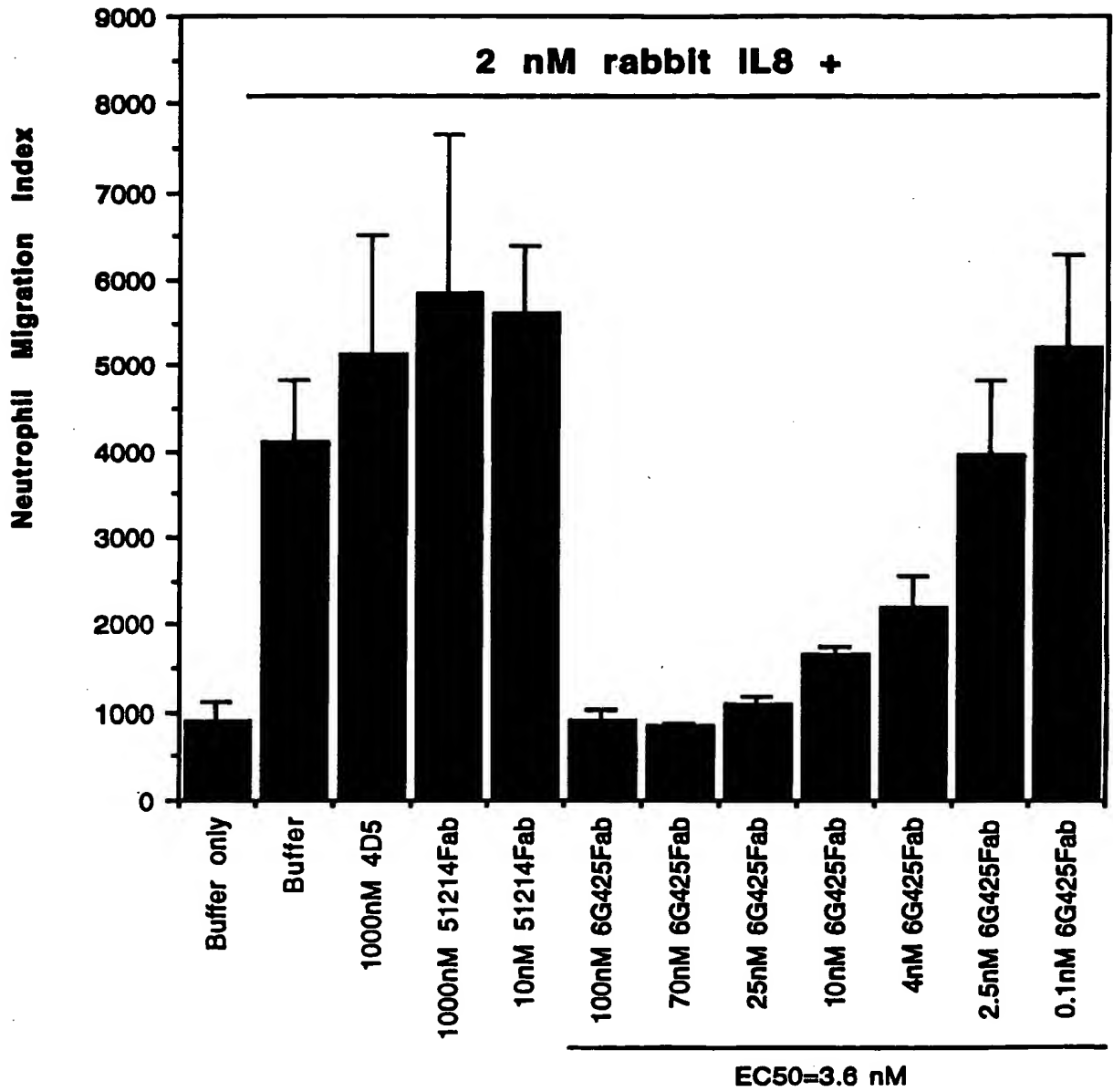


FIG. 7

Absorbance (405 nm)

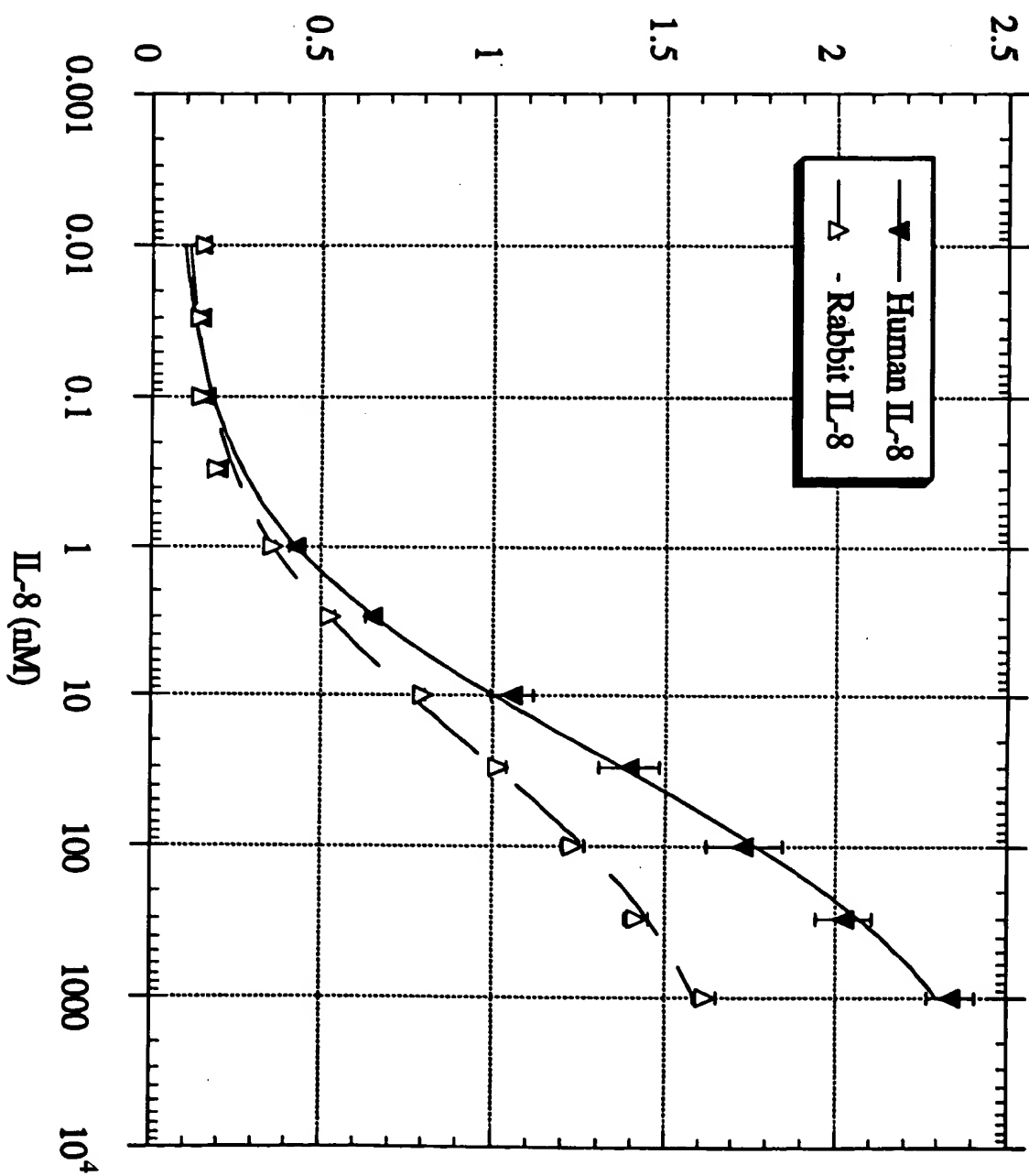


FIG. 8

% IL-8-Stimulated Elastase Release

FIG. 9

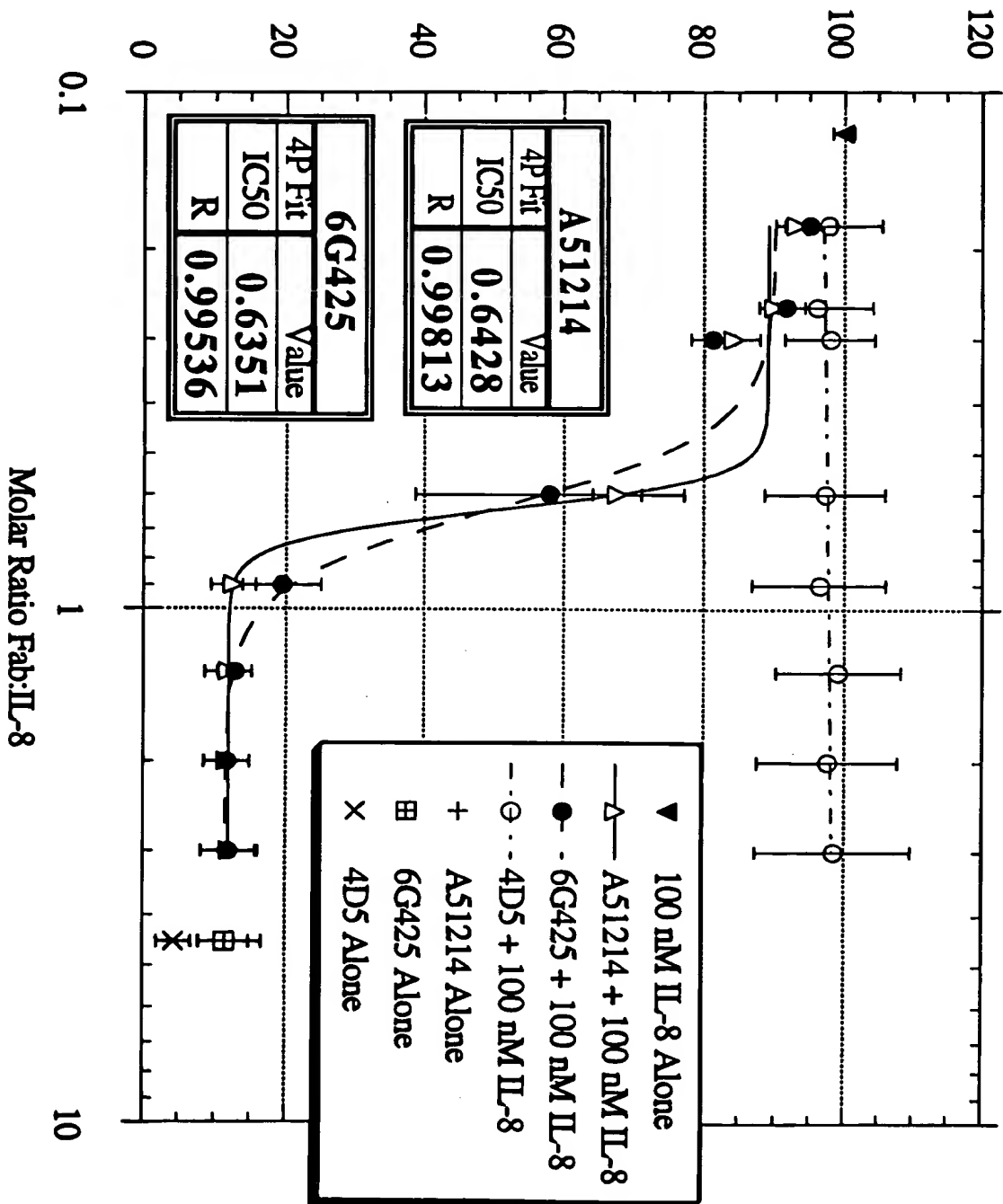
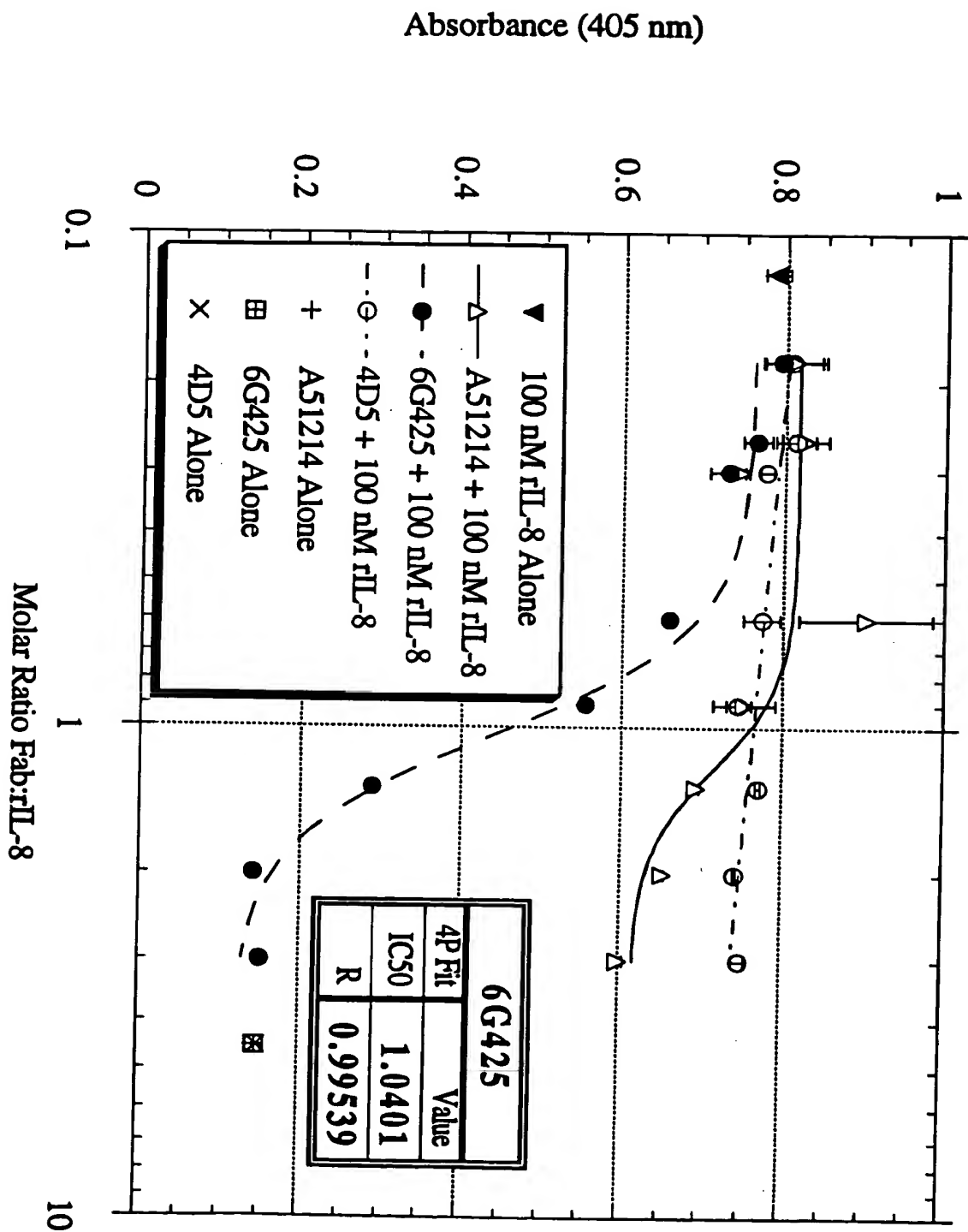


FIG. 10



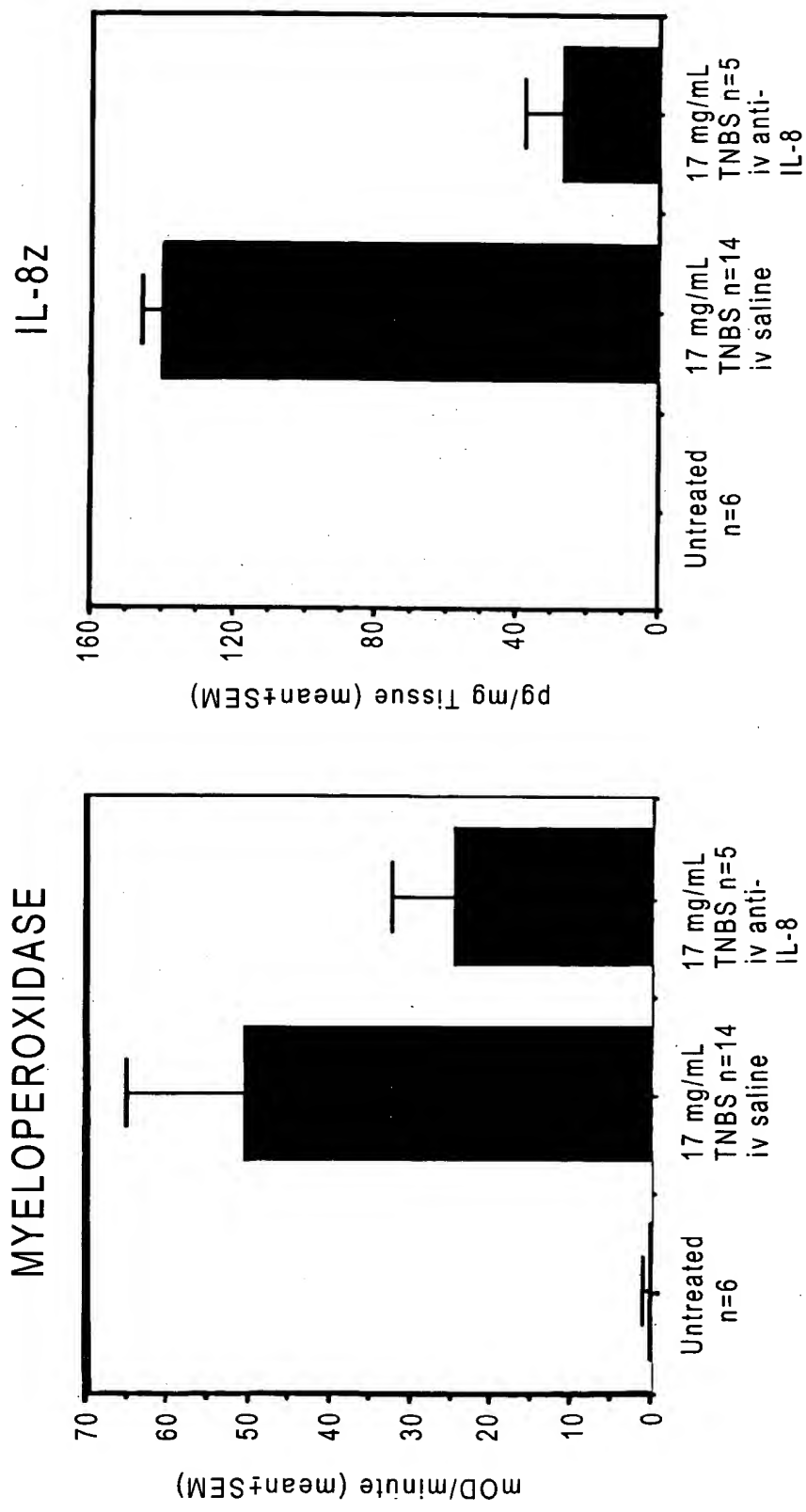


FIG. 11A

FIG. 11B

COLON WEIGHT

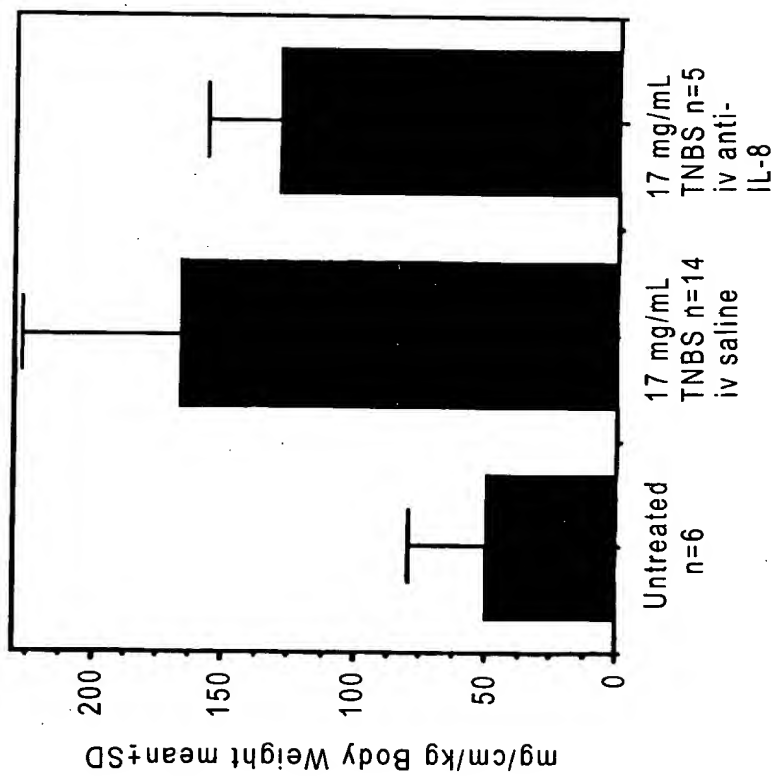


FIG. 11C

GROSS INFLAMMATION

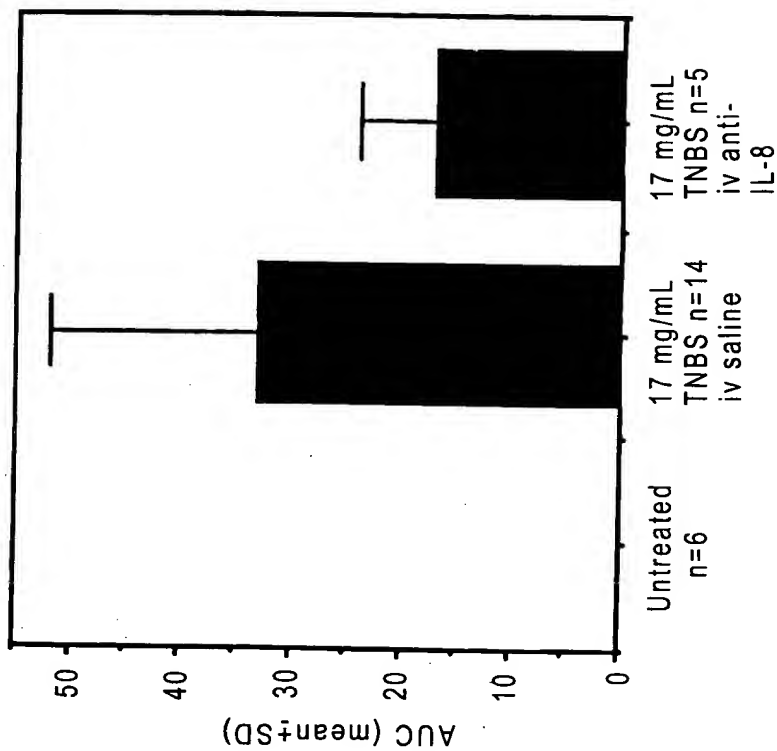


FIG. 11D

EDEMA

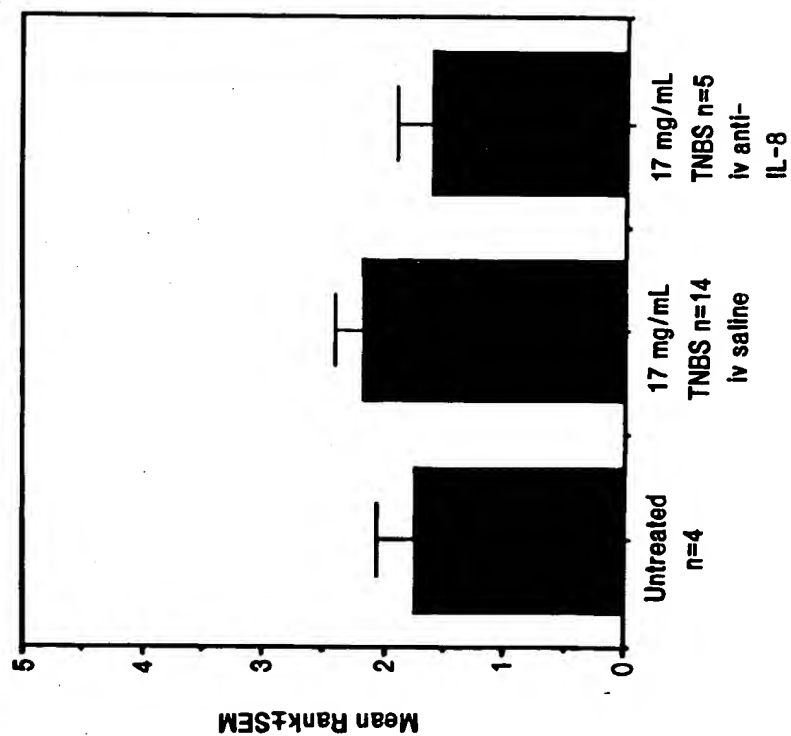


FIG. 11E

EXTENT OF NECROSIS

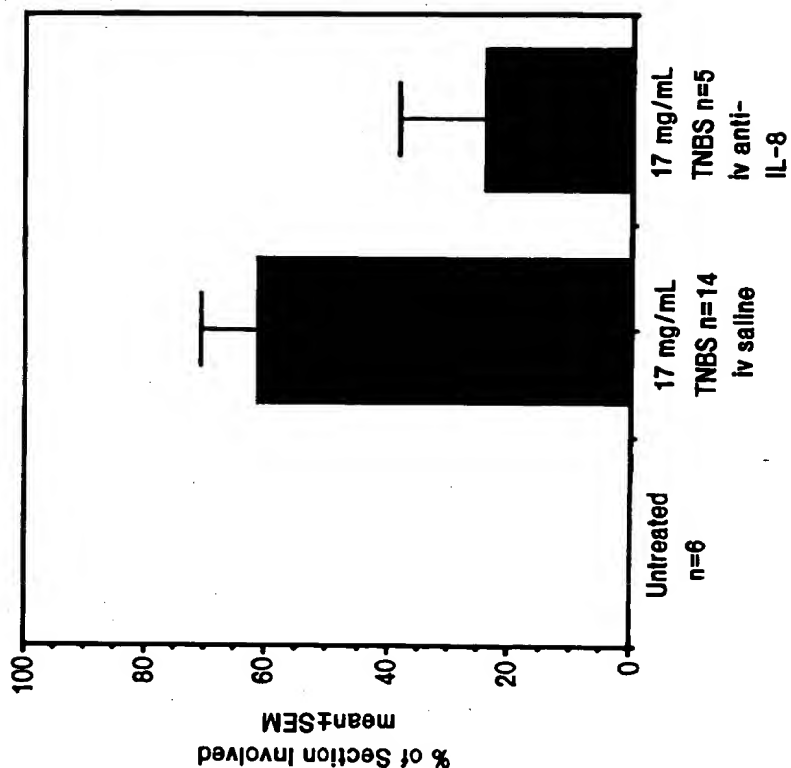


FIG. 11F

SEVERITY OF NECROSIS

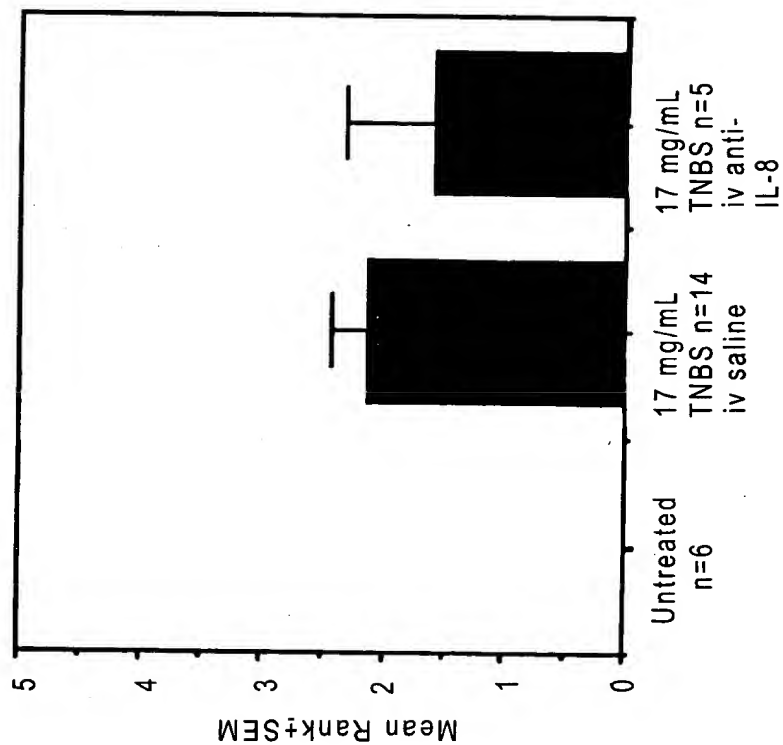


FIG. 11G

NEUTROPHIL MARGINATION

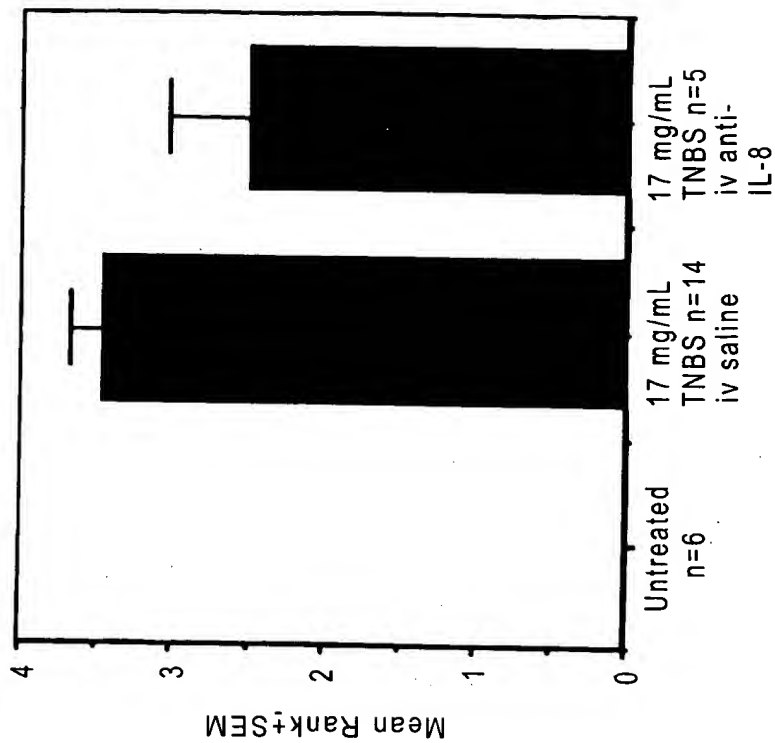


FIG. 11H

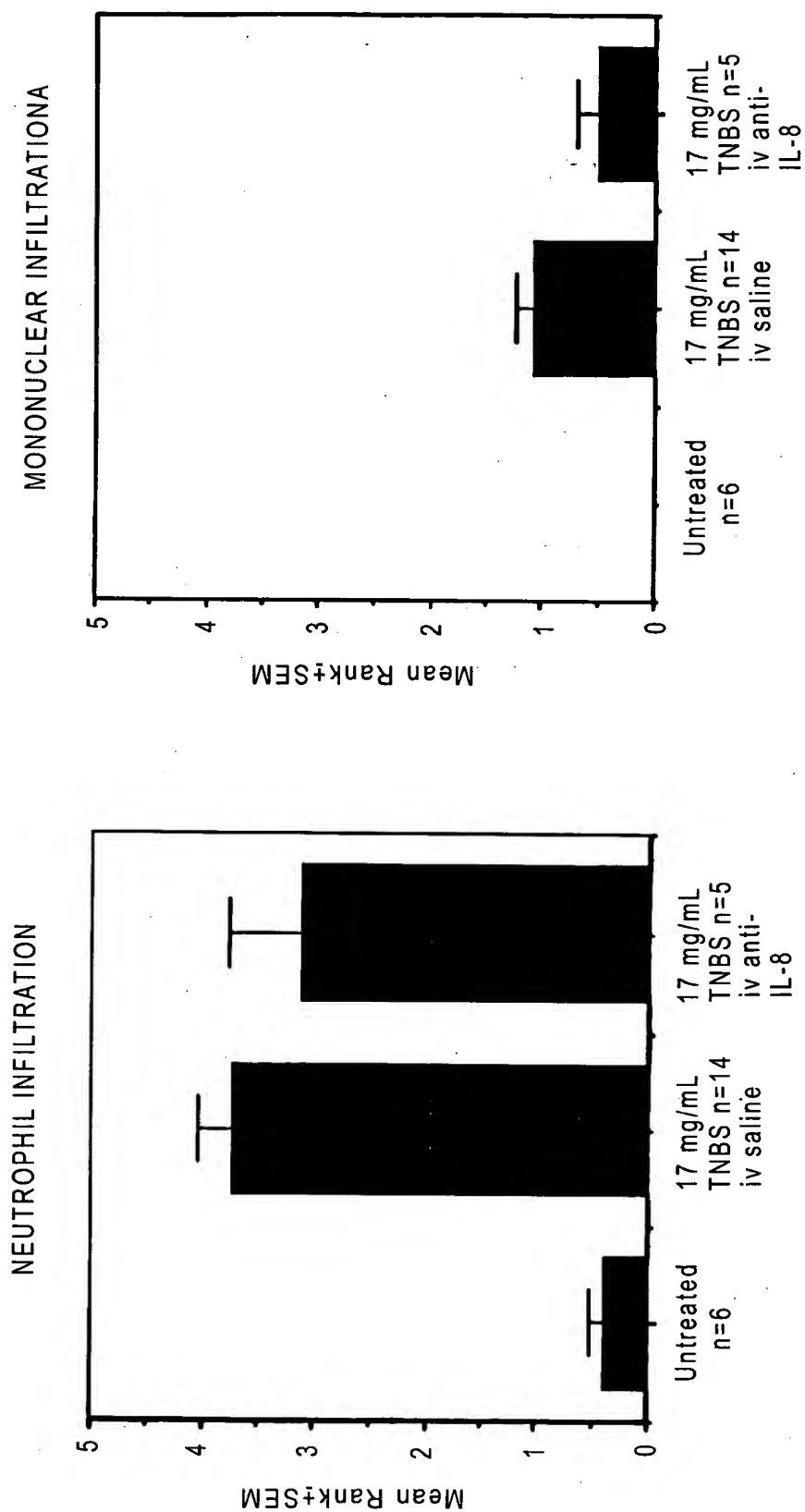
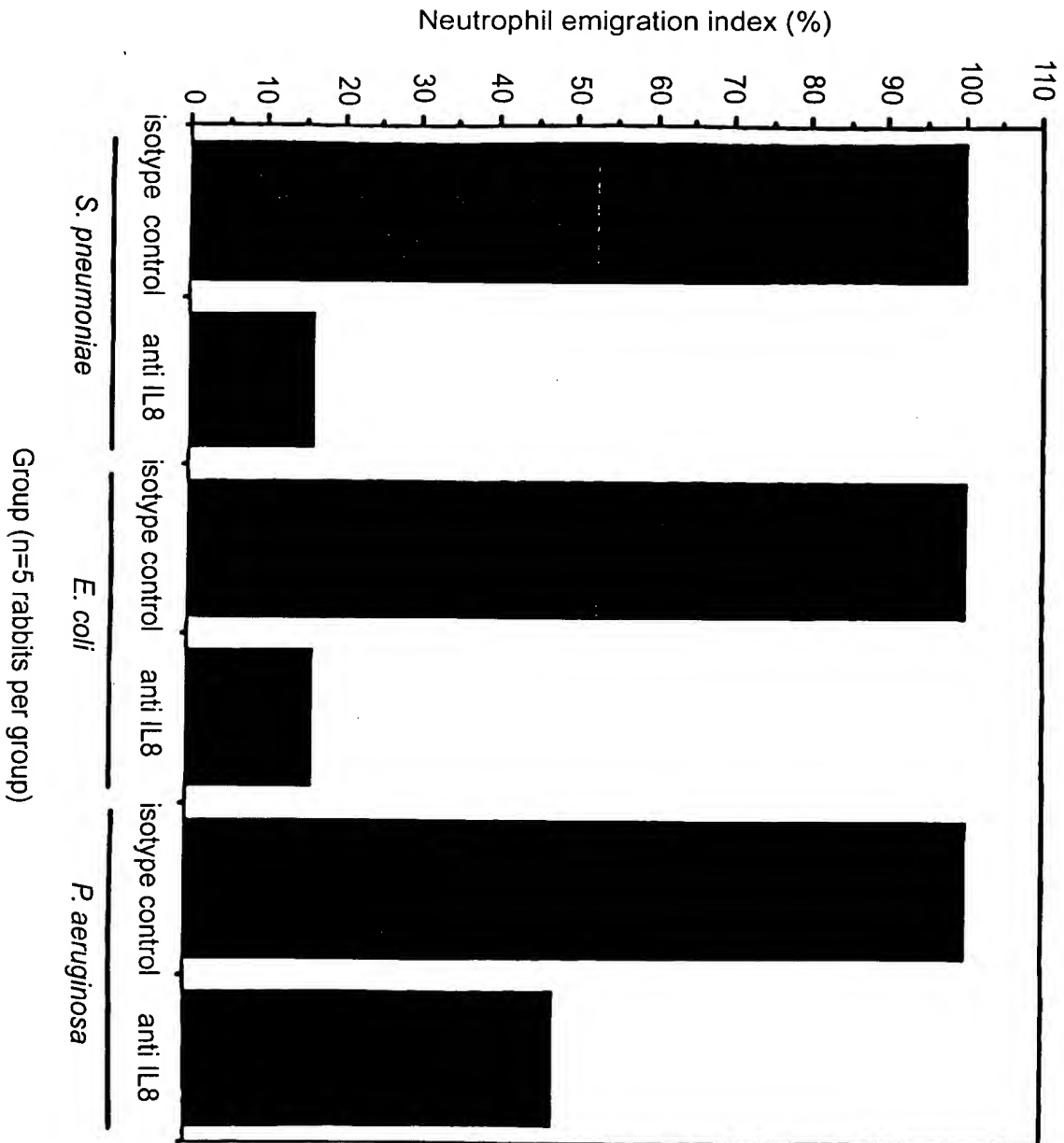


FIG. 11I

FIG. 11J



FIG. 12





Light Chain Primers:

MKLC-1, 22mer

5' CAGTCCAACCTGTTTCAGGACGCC 3'

MKLC-2, 22mer

5' GTGCTGCTCATGCTGTAGGTGC 3'

MKLC-3, 23mer

5' GAAGTTGATGTCTTGTGAGTGGC 3'

Heavy Chain Primers:

IGG2AC-1, 24mer

5' GCATCCTAGAGTCACCGAGGAGCC 3'

IGG2AC-2, 22mer

5' CACTGGCTCAGGGAAATAACCC 3'

IGG2AC-3, 22mer

5' GGAGAGCTGGGAAGGTGTGCAC 3'

FIG. 13



Light chain forward primer

SL001A-2 35 mer

5' ACAAACGCGTACGCT GACATCGTCATGACCCAGTC 3'
 T T T
 A

Light chain reverse primer

SL001B 37 mer

5' GCTCTTCGAATG GTGGGAAGATGGATACAGTTGGTGC 3'

FIG. 14



Heavy chain forward primer

SL002B 39 mer

5' CGATGGGCCCCG ATAGACCGATGGGGCTGTTGTTTTGGC 3'

T C
G
A

Heavy chain reverse primer

SL002B 39-MER

5' CGATGGGCCCCG ATAGACCGATGGGGCTGTTGTTTTGGC 3'

T
A
G

FIG. 15



1 GACATTGTCA TGACACAGTC TCAAAAATTC ATGTCCACAT CAGTAGGAGA CAGGGTCAGC
CTGTAACAGT ACTGTGTCAG AGTTTTTAAG TACAGGTGTA GTCATCCTCT GTCCCAGTCG
1 D I V M T Q S Q K F M S T S V G D R V S

61 GTCACCTGCA AGGCCAGTCA GAATGTGGT ACTAATGTAG CCTGGTATCA ACAGAAACCA
CAGTGGACGT TCCGGTCAGT CTTACACCCA TGATTACATC GGACCATAGT TGTCCTTTGGT
21 V T C K A S O N V G T N V A W Y Q Q K P
* * * * *

CDR #1

121 GGGCAATCTC CTAAGCACT GATTACTCG TCATCCTACC GGTACAGTGG AGTCCCTGAT
CCCGTTAGAG GATTTCGTGA CTAATGAGC AGTAGGATGG CCAATGTCACC TCAGGGACTA
41 G Q S P K A L I Y S S Y R Y S G V P D
* * * * *

CDR #2

181 CGCTTCACAG GCAGTGGATC TGGGACAGAT TTCACTCTCA CCATCAGCCA TGTGCAGTCT
GCGAAGTGTC CGTCACCTAG ACCCTGTCTA AAGTGAGAGT GGTAGTCGGT ACACGTCAGA
61 R F T G S G S G T D F T L T I S H V Q S

241 GAAAGACTGG CAGACTATTT CTGTCAGCAA TATAACATCT ATCCTCTCAC GTTCGGTCCCT
CTTCTGAACC GTCTGATAAA GACAGTCGTT ATATTGTAGA TAGGAGAGTG CAAGCCAGGA
81 E D L A D Y F C Q Q X N I Y P L T F G P
* * * * *

CDR #3

301 GGGACCAAGC TGGAGTTGAA ACGGGTGAT GCTGCACCAC CAACGTGTATC CATCTTCCCA
CCCTGGTTCG ACCTCAACTT TGCCCGACTA CGACGTGGTG GTTGACATAG GTAGAAGGGT
101 G T K L E L K R A D A A P P T V S I F P

BstBI

361 CCATTCGAA

GGTAAGCTT

121 P F E

FIG. 16



1 TTCTATTGCT ACAAACGCGT ACGCTGAGGT GCAGCTGGTG GAGTCTGGGG GAGGCTTAGT
AAGATAACGA TGTTTGCGCA TCGGACTCCA CGTCGACCAC CTCAGACCCC CTCCGAATCA
1 E V Q L V E S G G G L V

61 GCCGCCTGGA GGGTCCCTGA AACTCTCCTG TGCAGCCTCT GGATTCATAT TCAGTAGTTA
CGGCGGACCT CCCAGGGACT TTGAGAGGAC ACGTCGGAGA CCTAAGTATA AGTCATCAAT
13 P P G G S L K L S C A A S G F I F S S Y
* *

CDR #1

121 TGGCATGTCT TGGGTTCGCC AGACTCCAGG CAAGAGCCTG GAGTTGGTCG CAACCATTAA
ACCGTACAGA ACCCAAGCGG TCTGAGGTCC GTTCTCGGAC CTCAACCAGC GTTGGTAATT
33 G M S W V R Q T P G K S L E L V A T I N
* * *

181 TAATAATGGT GATAGCACCT ATTATCCAGA CAGTGTGAAG GGCCGATTCA CCATCTCCCG
ATTATTACCA CTATCGTGGA TAATAGGTCT GTCACACTTC CCGGCTAAGT GGTAGAGGGC
53 N N G D S T Y Y P D S V K G R F T I S R
* * * * *

CDR #2

241 AGACAATGCC AAGAACACCC TGTACCTGCA AATGAGCAGT CTGAAGTCTG AGGACACAGC
TCTGTTACGG TTCTTGTGGG ACATGGACGT TTA CTGTCG GACTTCAGAC TCCTGTGTCG
73 D N A K N T L Y L Q M S S L K S E D T A

301 CATGTTTTAC TGTGCAAGAG CCCTCATTAG TTCGGCTACT TGGTTTGGTT ACTGGGGCCA
GTACAAAATG ACACGTTCTC GGGAGTAATC AAGCCGATGA ACCAAACCAA TGACCCCGGT
93 M F Y C A R A L I S S A T W F G Y W G Q
* * * * *

CDR #3

361 AGGGACTCTG GTCAGTGTCT CTGCAGCCAA AACAAACAGCC CCATCTGTCT
TCCCTGAGAC CAGTGACAGA GACGTCGGTT TTGTTGTCGG GGTAGACAGA
113 G T L V T V S A A K T T A P S V Y

ApaI

411 ATCCGGG
TAGGCCC

130 P

FIG. 17



VL.front 31-MER

5' ACAAACGCGTACGCTGATATCGTCATGACAG 3'
VL.rear 31-MER

5' GCAGCATCAGCTCTTCGAAGCTCCAGCTTGG 3'

VH.front.SPE 21-MER

5' CCACTAGTACGCAAGTTCACG 3'

VH.rear 33-MER

5' GATGGGCCCTTGGTGGAGGCTGCAGAGACAGTG 3'

FIG. 18



1 ATGAAGAAGA ATATCGCATT TCTTCTTGCA TCTATGTTTCG TTTTCTCTAT TGCTACAAAC
TACTTCTTCT TATAGCGTAA AGAAGAACGT AGATACAAGC AAAAAAGATA ACGATGTTTG
-23 M K K N I A F L L A S M F V F S I A T N

61 GCGTACGCTG ATATCGTCAT GACACAGTCT CAAAAATTCA TGTCCACATC AGTAGGAGAC
CGCATGCGAC TATAGCAGTA CTGTGTCAGA GTTTTAAAGT ACAGGTGTAG TCATCCTCTG
-3 A Y A D I V M T Q S Q K F M S T S V G D

121 AGGGTCAGCG TCACCTGCAA GGCCAGTCAG AATGTGGGTA CTAATGTAGC CTGGTATCAA
TCCCAGTCGC AGTGGACGTT CCGGTCAGTC TTACACCCAT GATTACATCG GACCATAGTT
18 R V S V T C K A S O N V G T N V A W Y Q
* * * * *
CDR #1

181 CAGAAACCAG GGCAATCTCC TAAAGCACTG ATTTACTCGT CATCCTACCG GTACAGTGGA
GTCTTTGGTC CCGTTAGAGG ATTTCTGAC TAAATGAGCA GTAGGATGGC CATGTCACCT
38 Q K P G Q S P K A L I Y S S S Y R Y S G
* * * * *
CDR #2

241 GTCCCTGATC GCTTCACAGG CAGTGGATCT GGGACAGATT TCACTCTCAC CATCAGCCAT
CAGGGACTAG CGAAGTGTCC GTCACCTAGA CCCTGTCTAA AGTGAGAGTG GTAGTCGGTA
58 V P D R F T G S G S G T D F T L T I S H

301 GTGCAGTCTG AAGACTTGGC AGACTATTTT TGTCAGCAAT ATAACATCTA TCCTCTCACG
CACGTCAGAC TTCTGAACCG TCTGATAAAG ACAGTCGTTA TATTGTAGAT AGGAGAGTGC
78 V Q S E D L A D Y F C Q Q Y N I Y P L T
* * * * *
CDR #3

BstBI

361 TTCGGTCCTG GGACCAAGCT GGAGCTTCGA AGAGCTGTGG CTGCACCATC TGTCTTCATC
AAGCCAGGAC CCTGGTTCGA CCTCGAAGCT TCTCGACACC GACGTGGTAG ACAGAAGTAG
98 F G P G T K L E L R R A V A A P S V F I

421 TTCCCGCCAT CTGATGAGCA GTTGAAATCT GGAAGTCTT CTGTTGTGTG CCTGCTGAAT
AAGGGCGGTA GACTACTCGT CAACTTTAGA CCTTGACGAA GACAACACAC GGACGACTTA
118 F P P S D E Q L K S G T A S V V C L L N

481 AACTTCTATC CCAGAGAGGC CAAAGTACAG TGGAAGGTGG ATAACGCCCT CCAATCGGGT
TTGAAGATAG GGTCTCTCCG GTTTCATGTC ACCTTCCACC TATTGCGGGA GGTTAGCCCA
138 N F Y P R E A K V Q W K V D N A L Q S G

541 AACTCCCAGG AGAGTGTAC AGAGCAGGAC AGCAAGGACA GCACCTACAG CCTCAGCAGC
TTGAGGGTCC TCTCACAGTG TCTCGTCTCG TCGTTCTCTGT CGTGGATGTC GGAGTCGTGC
158 N S Q E S V T E Q D S K D S T Y S L S S

601 ACCCTGACGC TGAGCAAAGC AGACTACGAG AAACACAAAG TCTACGCCTG CGAAGTCACC
TGGGACTGCG ACTCGTTTCG TCTGATGCTC TTTGTGTTTC AGATGCGGAC GCTTCAGTGG
178 T L T L S K A D Y E K H K V Y A C E V T

661 CATCAGGGCC TGAGCTCGCC CGTCACAAAG AGCTTCAACA GGGGAGAGTG
GTAGTCCCGG ACTCGAGCGG GCAGTGTTTC TCGAAGTTGT CCCCTCTCAC
198 H Q G L S S P V T K S F N R G E C

711 TTAA
AATT
216 O

FIG. 19



1 ATGAAAAGA ATATCGCATT TCTTCTTGCA TCTATGTTTCG TTTTTCCTAT TGCTACAAAC
TACTTTTTCT TATAGCGTAA AGAAGAACGT AGATAACAAGC AAAAAAGATA ACGATGTTTG
-23 M K K N I A F L L A S M F V F S I A T N

61 GCGTACGCTG AGGTGCAGCT GGTGGAGTCT GGGGGAGGCT TAGTGCCGCC TGGAGGGTCC
CGCATGCGAC TCCACGTCGA CCACCTCAGA CCCCTCCGA ATCACGGCGG ACCTCCCAGG
-3 A Y A E V Q L V E S G G G L V P P G G S

121 CTGAAACTCT CCTGTGCAGC CTCTGGATTCT ATATTAGTA GTTATGGCAT GTCTTGGGTT
GACTTTGAGA GGACACGTCG GAGACCTAAG TATAAGTCAT CAATACCGTA CAGAACCCAA
18 L K L S C A A S G F I F S S Y G M S W V
* * * *

CDR #1

181 CGCCAGACTC CAGGCAAGAG CCTGGAGTTG GTCGCAACCA TTAATAATAA TGGTGATAGC
GCGGTCTGAG GTCCGTTCTC GGACCTCAAC CAGCGTTGGT AATTATTATT ACCACTATCG
38 R Q T P G K S L E L V A T I N N N G D S
* * * * *

241 ACCTATTATC CAGACAGTGT GAAGGGCCGA TTCACCATCT CCCGAGACAA TGCCAAGAAC
TGGATAATAG GTCTGTCACA CTTCCCGGCT AAGTGGTAGA GGGCTCTGTT ACGGTTCTTG
58 T Y Y P D S V K G R F T I S R D N A K N
* * * * *

CDR #2

301 ACCCTGTACC TGCAAATGAG CAGTCTGAAG TCTGAGGACA CAGCCATGTT TTAAGTGTGCA
TGGGACATGG ACGTTTACTC GTCAGACTTC AGACTCCTGT GTCGGTACAA AATGACACGT
78 T L Y L Q M S S L K S E D T A M F Y C A

361 AGAGCCCTCA TTAGTTCGGC TACTTGGTTT GGTACTGGG GCCAAGGGAC TCTGGTCACT
TCTCGGGAGT AATCAAGCCG ATGAACCAAA CCAATGACCC CGGTTCCCTG AGACCAAGTGA
98 R A L I S S A T W F G Y W G Q G T L V T
* * * * *

CDR #3

ApaI

421 GTCTCTGCAG CCTCCACCAA GGGCCCATCG GTCTTCCCCC TGGCACCCCTC CTCCAAGAGC
CAGAGACGTC GGAGGTGGTT CCCGGGTAGC CAGAAGGGGG ACCGTGGGAG GAGGTTCTCG
118 V S A A S T K G P S V F P L A P S S K S

481 ACCTCTGGGG GCACAGCGGC CCTGGGCTGC CTGGTCAAGG ACTACTTCCC CGAACCGGTG
TGGAGACCCC CGTGTGCGCCG GGACCCGACG GACCAAGTCC TGATGAAGGG GCTTGGCCAC
138 T S G G T A A L G C L V K D Y F P E P V

541 ACGGTGTCGT GGAAGTCAGG CGCCCTGACC AGCGGCGTGC ACACCTTCCC GGCTGTCCCTA
TGCCACAGCA CCTTGAGTCC GCGGGACTGG TCGCCGCACG TGTGGAAGGG CCGACAGGAT
158 T V S W N S G A L T S G V H T F P A V L

601 CAGTCCTCAG GACTCTACTC CCTCAGCAGC GTGGTGACCG TGCCCTCCAG CAGCTTGGGC
GTCAGGAGTC CTGAGATGAG GGAGTCGTCG CACCACTGGC ACGGGAGGTC GTCGAACCCG
178 Q S S G L Y S L S S V V T V P S S S L G

FIG. 20A



661 ACCCAGACCT ACATCTGCAA CGTGAATCAC AAGCCCAGCA ACACCAAGGT GGACAAGAAA
TGGGTCTGGA TGTAGACGTT GCACTTAGTG TTCGGGTCGT TGTGGTTCCA CCTGTTCTTT
198 T Q T Y I C N V N H K P S N T K V D K K

721 GTTGAGCCCA AATCTTGTGA CAAAACTCAC ACATGA
CAACTCGGGT TTAGAACACT GTTTTGAGTG TGTACT
218 V E P K S C D K T H T O

FIG. 20B



Light Chain Primers:

MKLC-1, 22mer

5' CAGTCCAACCTGTTTCAGGACGCC 3'

MKLC-2, 22mer

5' GTGCTGCTCATGCTGTAGGTGC 3'

MKLC-3, 23mer

5' GAAGTTGATGTCTTGTGAGTGGC 3'

Heavy Chain Primers:

IGG2AC-1, 24mer

5' GCATCCTAGAGTCACCGAGGAGCC 3'

IGG2AC-2, 22mer

5' CACTGGCTCAGGGAAATAACCC 3'

IGG2AC-3, 22mer

5' GGAGAGCTGGGAAGGTGTGCAC 3'

FIG. 21



Light chain forward primer

6G4.light.Nsi 36-MER

5' CCAATGCATACGCT GAC ATC GTG ATG ACC CAG ACC CC 3'
 T T T T
 A A

Light chain reverse primer

6G4.light.Mun 35-MER

5' AGA TGT CAA TTG CTC ACT GGA TGG TGG GAA GAT GG 3'

FIG. 22



Heavy chain forward primer

6G4.heavy.Mlu 32-MER

5' CAAACGCGTACGCT GAG ATC CAG CTG CAG CAG 3'
 T C

Heavy chain reverse primer

SL002B 39-MER

5' CGATGGGCCCCG ATAGACCGATGGGGCTGTTGTTTGGC 3'
 T
 A
 G

FIG. 23



70 G ATATCGTGAT GACACAGACA CCACTCTCCC TGCCTGTCAG TCTTGGAGAT
C TATAGCACTA CTGTGTCTGT GGTGAGAGGG ACGGACAGTC AGAACCTCTA
1 D I V M T Q T P L S L P V S L G D

121 CAGGCCTCCA TCTCTTGCAG ATCTAGTCAG AGCCTTGTAC ACGGTATTGG AAACACCTAT
GTCCGGAGGT AGAGAACGTC TAGATCAGTC TCGGAACATG TGCCATAACC TTTGTGGATA
18 Q A S I S C R S S O S L V H G I G N T Y
* * * * * * * * * * * * * *

CDR #1

181 TTACATTGGT ACCTGCAGAA GCCAGGCCAG TCTCCAAAGC TCCTGATCTA CAAAGTTTCC
AATGTAACCA TGGACGTCTT CCGTCCGGTC AGAGGTTTCG AGGACTAGAT GTTTCAAAGG
38 L H W Y L Q K P G Q S P K L L I Y K V S
* * * * * * * *

CDR #2

241 AACCGATTTT CTGGGGTCCC AGACAGGTTT AGTGGCAGTG GATCAGGGAC AGATTTTACA
TTGGCTAAAA GACCCAGGG TCTGTCCAAG TCACCGTCAC CTAGTCCCTG TCTAAAGTGT
58 N R F S G V P D R F S G S G S G T D F T
* * * * *

301 CTCAGGATCA GCAGAGTGGA GGCTGAGGAT CTGGGACTTT ATTTCTGCTC TCAAAGTACA
GAGTCCTAGT CGTCTCACCT CCGACTCCTA GACCCTGAAA TAAAGACGAG AGTTTCATGT
78 L R I S R V E A E D L G L Y F C S Q S T
* * * * *

CDR #3

361 CATGTTCCGC TCACGTTCCG TGCTGGGACC AAGCTGGAGC TGAAACGGGC TGATGCTGCA
GTACAAGGCG AGTGCAAGCC ACGACCTGG TTCGACCTCG ACTTTGCCCG ACTACGACGT
98 H V P L T F G A G T K L E L K R A D A A
* * * * *

MunI

421 CCAACTGTAT CCATCTTCCC ACCATCCAGT GAGCAATTGA
GGTTGACATA GGTAGAAGGG TGGTAGGTCA CTCGTTAAC T
118 P T V S I F P P S S E Q L K

FIG. 24



70 G AGATTCAGCT GCAGCAGTCT GGACCTGAGC TGATGAAGCC TGGGGCTTCA
C TCTAAGTCGA CGTCGTCAGA CCTGGACTCG ACTACTTCGG ACCCCGAAGT
1 E I Q L Q Q S G P E L M K P G A S

121 GTGAAGATAT CCTGCAAGGC TTCTGGTTAT TCATTCAGTA GCCACTACAT GCACTGGGTG
CACTTCTATA GGACGTTCCG AAGACCAATA AGTAAGTCAT CGGTGATGTA CGTGACCCAC
18 V K I S C K A S G Y S F S S H Y M H W V
* * * * *

CDR #1

181 AAGCAGAGCC ATGGAAAGAG CCTTGAGTGG ATTGGCTACA TTGATCCTTC CAATGGTGAA
TTCGTCTCGG TACCTTTCTC GGAAGTCACC TAACCGATGT AACTAGGAAG GTTACCACCT
38 K Q S H G K S L E W I G Y I D P S N G E
* * * * *

CDR #2

241 ACTACTTACA ACCAGAAATT CAAGGGCAAG GCCACATTGA CTGTAGACAC ATCTTCCAGC
TGATGAATGT TGGTCTTTAA GTTCCCGTTC CGGTGTAAGT GACATCTGTG TAGAAGGTCG
58 T T Y N Q K F K G K A T L T V D T S S S
* * * * *

301 ACAGCCAACG TGCATCTCAG CAGCCTGACA TCTGATGACT CTGCAGTCTA TTTCTGTGCA
TGTCGGTTGC ACGTAGAGTC GTCGGACTGT AGACTACTGA GACGTCAGAT AAAGACACGT
78 T A N V H L S S L T S D D S A V Y F C A

361 AGAGGGGACT ATAGATACAA CGGCGACTGG TTTTTCGATG TCTGGGGCGC AGGGACCACG
TCTCCCCTGA TATCTATGTT GCCGCTGACC AAAAAGCTAC AGACCCCGCG TCCCTGGTGC
98 R G D Y R Y N G D W F F D V W G A G T T
* * * * *

CDR #3

BstEII ApaI
421 GTCACCGTCT CCTCCGCCAA AACCGACAGC CCCATCGGTC TATCCGGGCC
CAGTGGCAGA GGAGGCGGAT TTGGCTGTCG GGGTAGCCAG ATAGGCCCGG
118 V T V S S A K T D S P I G L S G P

471 CATC
GTAG
135 I

FIG. 25



5' CTTGGTGGAGGCGGAGGAGACG 3'

Mutagenesis Primer for 6G425VL

DS/VF 38MER

5' GAAACGGGCTGTTGCTGCACCAACTGTATTCATCTTCC 3'

SYN.BstEII 31 MER

5' GTCACCGTCT CCTCCGCCTC CACCAAGGGC C 3'

SYN.Apa 22 MER

5' CTTGGTGGAGGCGGAGGAGACG 3'

FIG. 26



1 ATGAAGAAGA ATATCGCATT TCTTCTTGCA TCTATGTTTCG TTTTCTCTAT TGCTACAAAT
TACTTCTTCT TATAGCGTAA AGAAGAACGT AGATACAAGC AAAAAAGATA ACGATGTTTA
-23 M K K N I A F L L A S M F V F S I A T N

61 GCATACGCTG ATATCGTGAT GACACAGACA CCACTCTCCC TGCCTGTCAG TCTTGGAGAT
CGTATGCGAC TATAGCACTA CTGTGTCTGT GGTGAGAGGG ACGGACAGTC AGAACCTCTA
-3 A Y A D I V M T Q T P L S L P V S L G D

121 CAGGCCTCCA TCTCTTGCGAG ATCTAGTCAG AGCCTTGTTAC ACGGTATTGG AAACACCTAT
GTCCGGAGGT AGAGAACGTC TAGATCAGTC TCGGAACATG TGCCATAACC TTTGTGGATA
18 Q A S I S C R S S O S L V H G I G N T Y
* * * * * * * * * * * * * * *

CDR #1

181 TTACATTGGT ACCTGCAGAA GCCAGGCCAG TCTCCAAAGC TCCTGATCTA CAAAGTTTCC
AATGTAACCA TGGACGTCTT CCGTCCGGTC AGAGGTTTCG AGGACTAGAT GTTTCAAAGG
38 L H W Y L Q K P G Q S P K L L I Y K V S
* * * * * * * *

CDR #2

241 AACCGATTTT CTGGGGTCCC AGACAGGTTT AGTGGCAGTG GATCAGGGAC AGATTTTACA
TTGGCTAATAA GACCCAGGG TCTGTCCAAG TCACCGTCAC CTAGTCCCTG TCTAAAGTGT
58 N R F S G V P D R F S G S G S G T D F T
* * * * *

301 CTCAGGATCA GCAGAGTGGA GGCTGAGGAT CTGGGACTTT ATTTCTGCTC TCAAAGTACA
GAGTCCTAGT CGTCTCACCT CCGACTCCTA GACCCTGAAA TAAAGACGAG AGTTTCATGT
78 L R I S R V E A E D L G L Y F C S Q S T
* * * * *

CDR #3

361 CATGTTCCGC TCACGTTCCG TGCTGGGACC AAGCTGGAGC TGAAACGGGC TGTGCTGCA
GTACAAGGCG AGTGCAAGCC ACGACCCTGG TTCGACCTCG ACTTTGCCCG ACAACGACGT
98 H V P L T F G A G T K L E L K R A V A A
* * * * *

421 CCAACTGTAT TCATCTTCCC ACCATCCAGT GAGCAATTGA AATCTGGAAC TGCCTCTGTT
GGTTGACATA AGTAGAAGGG TGGTAGGTCA CTCGTAACT TTAGACCTTG ACGGAGACAA
118 P T V F I F P P S S E Q L K S G T A S V

481 GTGTGCCTGC TGAATAACTT CTATCCCAGA GAGGCCAAAG TACAGTGGAA GGTGGATAAC
CACACGGACG ACTTATTGAA GATAGGGTCT CTCCGGTTTC ATGTACACCTT CCACCTATTG
138 V C L L N N F Y P R E A K V Q W K V D N

541 GCCCTCCAAT CGGGTAACTC CCAGGAGAGT GTCACAGAGC AGGACAGCAA GGACAGCACC
CGGGAGGTTA GCCCATTGAG GGTCTCTCA CAGTGTCTCG TCCTGTCTGT CCTGTCTGTG
158 A L Q S G N S Q E S V T E Q D S K D S T

601 TACAGCCTCA GCAGCACCTT GACGCTGAGC AAAGCAGACT ACGAGAAACA CAAAGTCTAC
ATGTCGGAGT CGTCGTGGGA CTGCGACTCG TTTCTGTCTGA TGCTCTTTGT GTTTCAGATG
178 Y S L S S T L T L S K A D Y E K H K V Y

FIG. 27A



661 GCCTGCGAAG TCACCCATCA GGGCCTGAGC TCGCCCGTCA CAAAGAGCTT CAACAGGGGA
CGGACGCTTC AGTGGGTAGT CCCGACTCG AGCGGCAGT GTTCTCGAA GTTGTCCTCCT
198 A C E V T H Q G L S S P V T K S F N R G

721 GAGTGTAA
CTCACAATT
218 E C O

FIG. 27B



1 ATGAAAAAGA ATATCGCATT TCTTCTTGCA TCTATGTTTCG TTTTTCCTAT TGCTACAAAC
TACTTTTTTCT TATAGCGTAA AGAAGAACGT AGATACAAGC AAAAAAGATA ACGATGTTTG
-23 M K K N I A F L L A S M F V F S I A T N

61 GCGTACGCTG AGATTTCAGCT GCAGCAGTCT GGACCTGAGC TGATGAAGCC TGGGGCTTCA
CGCATGCGAC TCTAAGTCGA CGTCGTCAGA CCTGGACTCG ACTACTTCGG ACCCCGAAGT
-3 A Y A E I Q L Q Q S G P E L M K P G A S

121 GTGAAGATAT CCTGCAAGGC TTCTGGTTAT TCATTTCAGTA GCCACTACAT GCACTGGGTG
CACTTCTATA GGACGTTCCG AAGACCAATA AGTAAGTCAT CGGTGATGTA CGTGACCCAC
18 V K I S C K A S G Y S F S S H Y M H W V
* * * * *

CDR #1

181 AAGCAGAGCC ATGGAAAGAG CCTTGAGTGG ATTGGCTACA TTGATCCTTC CAATGGTGAA
TTCGTCTCGG TACCTTCTC GGAACCTACC TAACCGATGT AACTAGGAAG GTTACCACTT
38 K Q S H G K S L E W I G Y I D P S N G E
* * * * *

CDR #2

241 ACTACTTACA ACCAGAAATT CAAGGGCAAG GCCACATTGA CTGTAGACAC ATCTTCCAGC
TGATGAATGT TGGTCTTTAA GTTCCCGTTC CGGTGTAAC TACATCTGTG TAGAAGGTCG
58 T T Y N Q K F K G K A T L T V D T S S S
* * * * *

301 ACAGCCAACG TGCATCTCAG CAGCCTGACA TCTGATGACT CTGCAGTCTA TTTCTGTGCA
TGTCGGTTGC ACGTAGAGTC GTCGGACTGT AGACTACTGA GACGTCAGAT AAAGACACGT
78 T A N V H L S S L T S D D S A V Y F C A

361 AGAGGGGACT ATAGATACAA CGGCGACTGG TTTTTCGATG TCTGGGGCGC AGGGACCACG
TCTCCCCTGA TATCTATGTT GCCGCTGACC AAAAAGCTAC AGACCCCGCG TCCCTGGTGC
98 R G D Y R Y N G D W F F D V W G A G T T
* * * * *

CDR #3

421 GTCACCGTCT CCTCCGCCTC CACCAAGGGC CCATCGGTCT TCCCCCTGGC ACCCTCCTCC
CAGTGGCAGA GGAGGCGGAG GTGGTTCCCG GGTAGCCAGA AGGGGGACCG TGGGAGGAGG
118 V T V S S A S T K G P S V F P L A P S S

481 AAGAGCACCT CTGGGGGCAC AGCGGCCCTG GGCTGCCTGG TCAAGGACTA CTTCCCCGAA
TTCTCGTGGA GACCCCGTG TCGCCGGGAC CCGACGGACC AGTTCCTGAT GAAGGGGCTT
138 K S T S G G T A A L G C L V K D Y F P E

541 CCGGTGACGG TGTCGTGGAA CTCAGGCGCC CTGACCAGCG GCGTGCACAC CTTCCCGGCT
GGCCACTGCC ACAGCACCTT GAGTCCGCGG GACTGGTCGC CGCACGTGTG GAAGGGCCGA
158 P V T V S W N S G A L T S G V H T F P A

601 GTCCTACAGT CCTCAGGACT CTACTCCCTC AGCAGCGTGG TGACCGTGCC CTCCAGCAGC
CAGGATGTCA GGAGTCCTGA GATGAGGGAG TCGTCGCACC ACTGGCACGG GAGGTCGTGC
178 V L Q S S G L Y S L S S V V T V P S S S

FIG. 28A



661 TTGGGCACCC AGACCTACAT CTGCAACGTG AATCACAAGC CCAGCAACAC CAAGGTGGAC
AACCCGTGGG TCTGGATGTA GACGTTGCAC TTAGTGTTCG GGTGTTGTG GTTCCACCTG
198 L G T Q T Y I C N V N H K P S N T K V D
721 AAGAAAGTTG AGCCCAATC TTGTGACAAA ACTCACACAT GA
TTCTTTCAAC TCGGGTTTAG AACACTGTTT TGAGTGTGTA CT
218 K K V E P K S C D K T H T O

FIG. 28B



Variable Light Chain Domain

	10	20	abcde	30	40
6G425	DI	VTQTPLSLP	VS	LG	DQASISCRSSQSLVHGIGNTYLHWYLQKPGQSPKLLIY
	#	#	#	#	#
F(ab)-1	DI	QMTQSPSSLSASV	GDRVTITCRSSQSLVHGIGNTYLHWYQQKPGKAPKLLIY		
					#
humkI	DI	QMTQSPSSLSASV	GDRVTITCRASKTI	-----	SKYLAWYQQKPGKAPKLLIY
					=====
					+++++
					L1

	50	60	70	80	90	100
6G425	YK	VS	NR	FS	GV	PDRFSDSGSGTDFTLRISRVEAEDLGLYFCSQSTHVPLTFGAGTKLELKR
		#	#		#	#
F(ab)-1	YK	VS	NR	FS	GV	PSRFRSGSGSGTDFTLTISLQPEDFATYYCSQSTHVPLTFGQGTKVEIKR
	#	#	#		#	#
humkI	Y	S	G	S	T	L
						=====
						+++++
						L2

	50	60	70	80	90	100
6G425	YK	VS	NR	FS	GV	PDRFSDSGSGTDFTLRISRVEAEDLGLYFCSQSTHVPLTFGAGTKLELKR
		#	#		#	#
F(ab)-1	YK	VS	NR	FS	GV	PSRFRSGSGSGTDFTLTISLQPEDFATYYCSQSTHVPLTFGQGTKVEIKR
	#	#	#		#	#
humkI	Y	S	G	S	T	L
						=====
						+++++
						L3

Variable Heavy Chain Domain

	10	20	30	40
6G425	EI	QLQ	QSGPELMKPGASVKISCKASGYSFSSHYMHVWKQSHGKSLEWI	
	#	#	#	#
F(ab)-1	EV	QLVESGGGLVQPGGSLRLS	CAASGYSFSSHYMHVWRQAPGKGLEWV	
			#	#
humIII	EV	QLVESGGGLVQPGGSLRLS	CAASGFSFTGHWMNVWRQAPGKGLEWV	
				=====
				+++++
				H1

	50	a	70	80	abc	90	100	110
6G425	GY	ID	PSNGETT	YNQKFKGKATLT	VDTSSTANVHLSSLTSDDS	AVYFCAARGDYRYNGDWFFDVWGAGT		
			#	#	#	#	#	#
F(ab)-1	GY	ID	PSNGETT	YNQKFKGRFTISR	DN	SKNTLYLQMN	SLRAEDTAVYYCAARGDYRYNGDWFFDVWGQGT	
	#	#	#	#	#	#	#	#
humIII	G	M	I	PSDSETRYADSVKGRFTISR	DN	SKNTLYLQMN	SLRAEDTAVYYCAARGIIFY-GTTYFDYWQGT	
								=====
								+++++
								H2

	50	a	70	80	abc	90	100	110
6G425	GY	ID	PSNGETT	YNQKFKGKATLT	VDTSSTANVHLSSLTSDDS	AVYFCAARGDYRYNGDWFFDVWGAGT		
			#	#	#	#	#	#
F(ab)-1	GY	ID	PSNGETT	YNQKFKGRFTISR	DN	SKNTLYLQMN	SLRAEDTAVYYCAARGDYRYNGDWFFDVWGQGT	
	#	#	#	#	#	#	#	#
humIII	G	M	I	PSDSETRYADSVKGRFTISR	DN	SKNTLYLQMN	SLRAEDTAVYYCAARGIIFY-GTTYFDYWQGT	
								=====
								+++++
								H3

FIG. 29

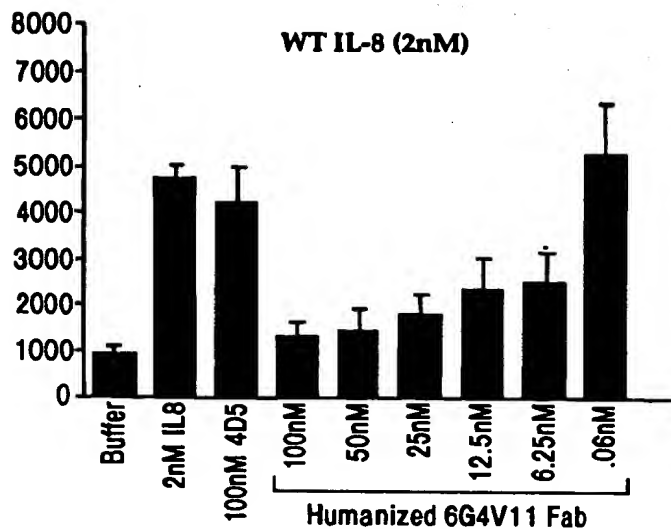


FIG. 30A

IC₅₀~12nM

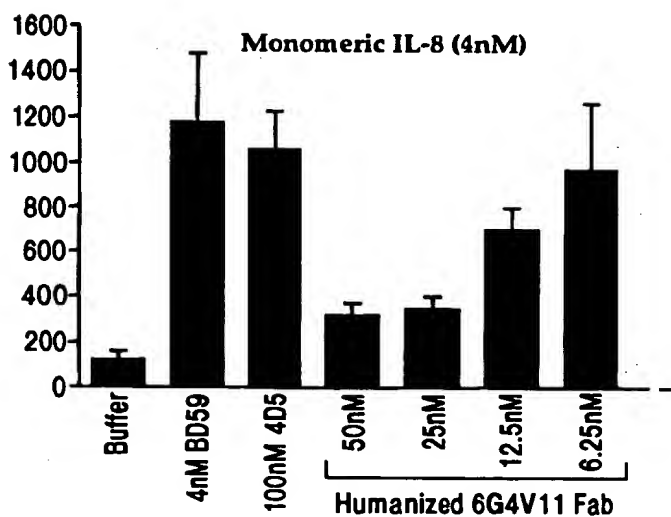


FIG. 30B

IC₅₀~15nM

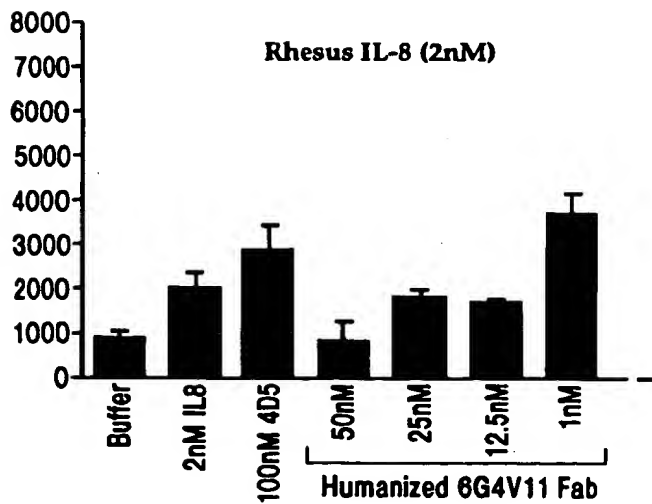


FIG. 30C

IC₅₀~22nM



Amino Acid Sequence of the humanized anti-IL-8 6G4.2.5V11 Light Chain

MKKNIAFLLASMFVFSIATNAYADIQMTQSPSSLSASVGDRTTITCRSSQSLVHGIGNTY
LHWYQQKPGKAPKLLIYKVSNNRFSGVPSRFSGSGGTDFTLTISSLQPEDFATYYCSQST
HVP LTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDN
ALQSGNSQESVTEQDSKDSSTLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG
EC

Amino Acid Sequence of the humanized anti-IL-8 6G4.2.5V11 Heavy Chain

MKKNIAFLLASMFVFSIATNAYAEVQLVQSGGGLVQPGGSLRLSCAASGYSFSSHYMH
WVRQAPGKGLEWVG YIDPSNGETTYNQKFKGRFTLSRDNSKNTAYLQMNSLRAEDTAVYY
CARGDYRYNGDWFFDWGQGT LVTVSSASTKGPSVFLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHHKPSNTK
VDKKVEPKSCDKTHT

Amino Acid Sequence of the peptide linker and M13 Phage Coat (gene-III)

SGGGSGGDFDYKMANANKGAMTENADENALQSDAKGKLDVATDYGAIDFGIDVVS
GLANGNGATGDFAGSSNSQMAQVGDGDN SPLMNNFRQYLP LPSLPQSV ECRPFVFSAGKPY
EFSIDCDKINLFRGVFAFLLYVATFMYVFTFANILRNKES

FIG. 31A



1 ATGAAAAAGA ATATCGCATT TCTTCTTGCA TCTATGTTTCG TTTTCTCTAT TGCTACAAAC
TACTTTTTCT TATAGCGTAA AGAAGAACGT AGATACAAGC AAAAAAGATA ACGATGTTTG
-23 M K K N I A F L L A S M F V F S I A T N

61 GCATACGCTG ATATCCAGAT GACCCAGTCC CCGAGCTCCC TGTCCGCCTC TGTGGGCGAT
CGTATGCGAC TATAGGTCTA CTGGGTCAGG GGCTCGAGGG ACAGGCGGAG ACACCCGCTA
-3 A Y A D I Q M T Q S P S S L S A S V G D

121 AGGGTCACCA TCACCTGCAG GTCAAGTCAA AGCTTAGTAC ATGGTATAGG TAACACGTAT
TCCCAGTGGT AGTGGACGTC CAGTTCAGTT TCGAATCATG TACCATATCC ACGATGCATA
18 R V T I T C R S S Q S L V H G I G N T Y

181 TTACACTGGT ATCAACAGAA ACCAGGAAAA GCTCCGAAAC TACTGATTTA CAAAGTATCC
AATGTGACCA TAGTTGTCTT TGGTCCTTTT CGAGGCTTTG ATGACTAAAT GTTTCATAGG
38 L H W Y Q Q K P G K A P K L L I Y K V S

241 AATCGATTCT CTGGAGTCCC TTCTCGCTTC TCTGGATCCG GTTCTGGGAC GGATTTCACT
TTAGCTAAGA GACCTCAGGG AAGAGCGAAG AGACCTAGGC CAAGACCCTG CCTAAAGTGA
58 N R F S G V P S R F S G S G S G T D F T

301 CTGACCATCA GCAGTCTGCA GCCAGAAGAC TTCGCAACTT ATTACTGTTT ACAGAGTACT
GACTGGTAGT CGTCAGACGT CGGTCTTCTG AAGCGTTGAA TAATGACAAG TGTCTCATGA
78 L T I S S L Q P E D F A T Y Y C S Q S T

361 CATGTCCCGC TCACGTTTGG ACAGGGTACC AAGGTGGAGA TCAAACGAAC TGTGGCTGCA
GTACAGGGCG AGTGCAAACC TGTCCTCATGG TTCCACCTCT AGTTTGCTTG ACACCGACGT
98 H V P L T F G Q G T K V E I K R T V A A

421 CCATCTGTCT TCATCTTCCC GCCATCTGAT GAGCAGTTGA AATCTGGAAC TGCTTCTGTT
GGTAGACAGA AGTAGAAGGG CGGTAGACTA CTCGTCAACT TTAGACCTTG ACGAAGACAA
118 P S V F I F P P S D E Q L K S G T A S V

481 GTGTGCCTGC TGAATAACTT CTATCCCAGA GAGGCCAAAG TACAGTGGAA GGTGGATAAC
CACACGGACG ACTTATTGAA GATAGGGTCT CTCCGGTTTC ATGTCACCTT CCACCTATTG
138 V C L L N N F Y P R E A K V Q W K V D N

541 GCCCTCCAAT CGGGTAACTC CCAGGAGAGT GTCACAGAGC AGGACAGCAA GGACAGCACC
CGGGAGGTTA GCCCATTGAG GGTCCCTCTCA CAGTGTCTCG TCCTGTCGTT CCTGTCGTGG
158 A L Q S G N S Q E S V T E Q D S K D S T

601 TACAGCCTCA GCAGCACCCCT GACGCTGAGC AAAGCAGACT ACGAGAAACA CAAAGTCTAC
ATGTCGGAGT CGTCGTGGGA CTGCGACTCG TTTCGTCTGA TGCTCTTTGT GTTTCAGATG
178 Y S L S S T L T L S K A D Y E K H K V Y

661 GCCTGCGAAG TCACCCATCA GGGCCTGAGC TCGCCCGTCA CAAAGAGCTT CAACAGGGGA
CGGACGCTTC AGTGGGTAGT CCCGGACTCG AGCGGGCAGT GTTCTCTGAA GTTGTCCCCT
198 A C E V T H Q G L S S P V T K S F N R G

721 GAGTGTTAAG CTGATCCTCT ACGCCGGACG CATCGTGGCC CTAGTACGCA ACTAGTCGTA
CTCACAATTC GACTAGGAGA TCGGGCCTGC GTAGCACCGG GATCATGCGT TGATCAGCAT
218 E C O

FIG. 31B



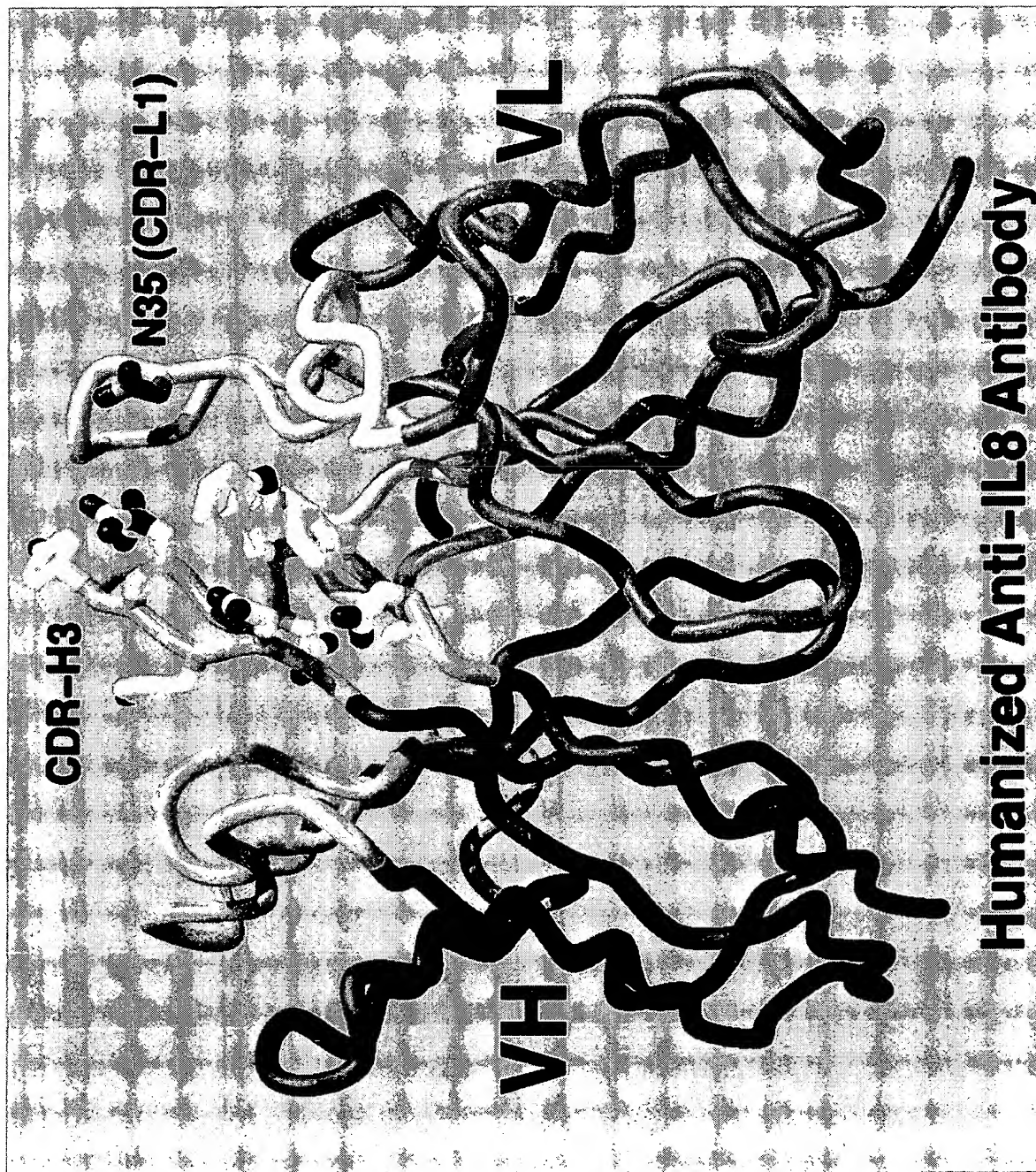
Amino Acid Sequence of the humanized anti-IL-8 6G4.2.5V19 Light Chain

MKKNIAFLLASMFVFSIATNAYADIQMTQSPSSLSASVGDRTTITCRSSQSLVHGIGNTY
LHWYQQKPGKAPKLLIYKVSNRFSGVPSRFSGSGGTDFTLTISSLQPEDFATVYCSQST
HVPLTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDN
ALQSGNSQESVTEQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG
EC

Amino Acid Sequence of the humanized anti-IL-8 6G4.2.5V19 Heavy Chain

MKKNIAFLLASMFVFSIATNAYAEVQLVESGGGLVQPGGSLRLSCAASGYSFSSHYMH
WVKQAPGKGLEWVGYYIDPSNGETTYNQKFKGRFTLSRDNSKNTAYLQMNSLRAEDTAVYY
CARGDYRYNGDWFFDVWGQGTLLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTK
VDKKVEPKSCDKTHT

FIG. 31C



Humanized Anti-IL8 Antibody

FIG. 32

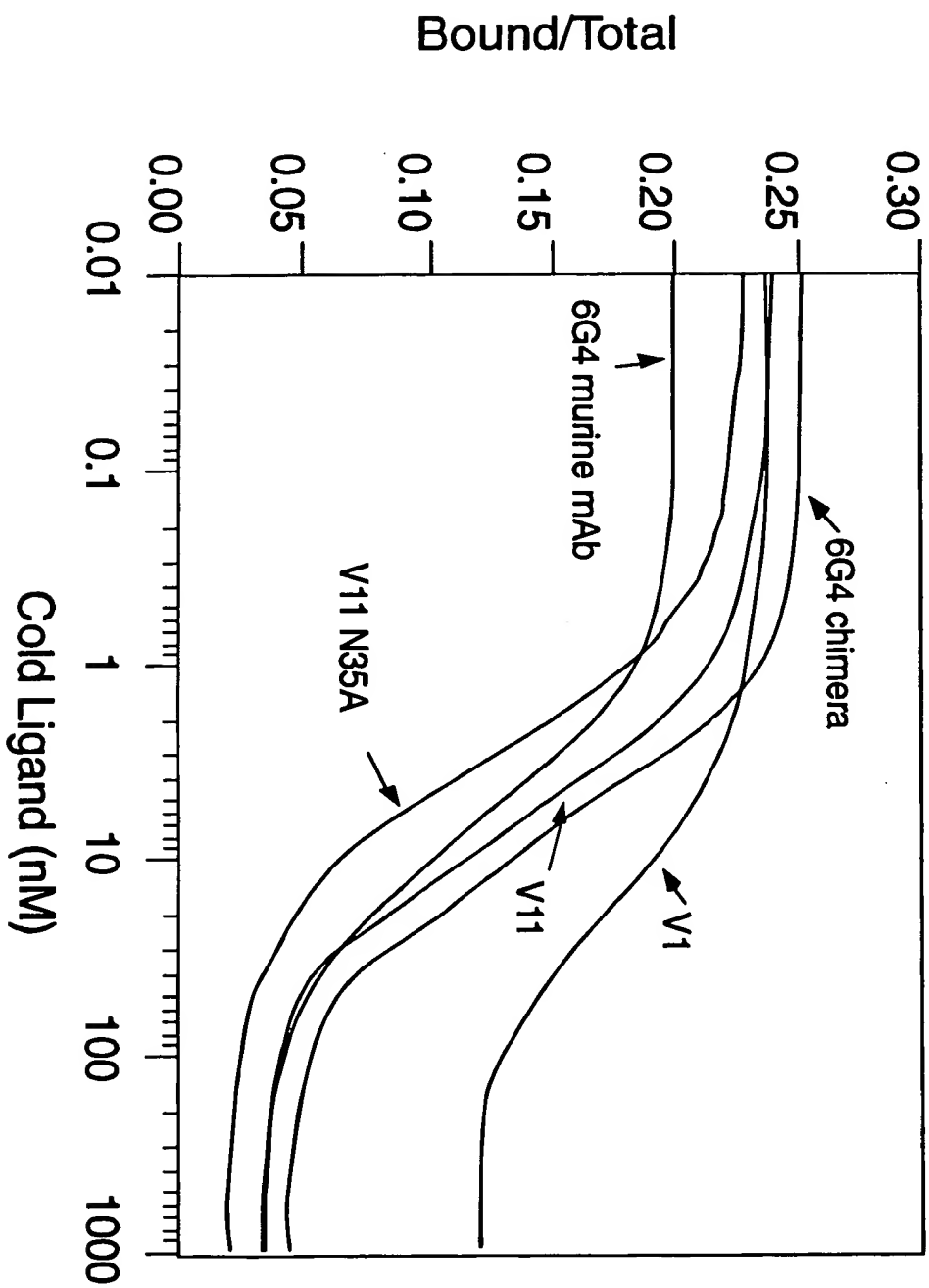


FIG. 33

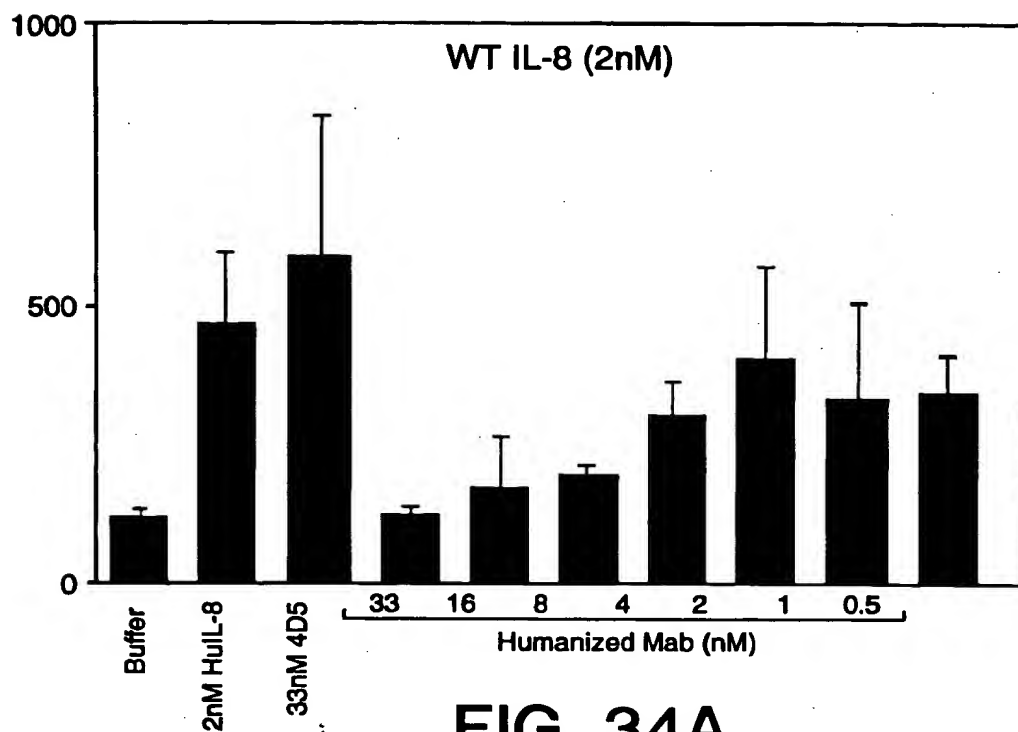


FIG. 34A

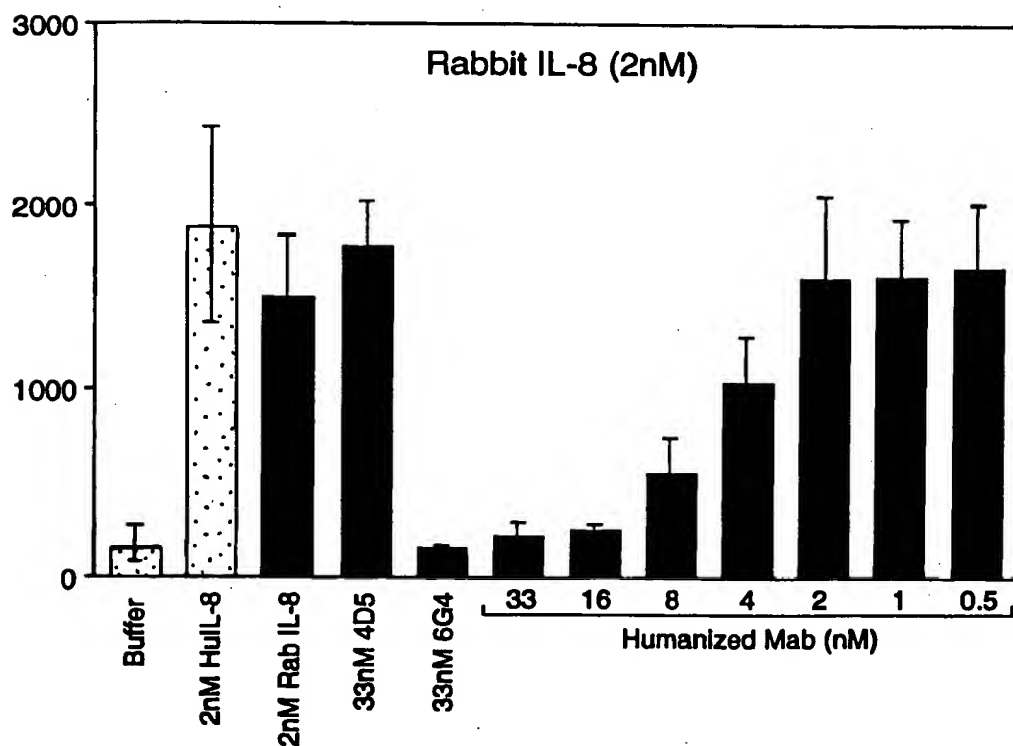


FIG. 34B

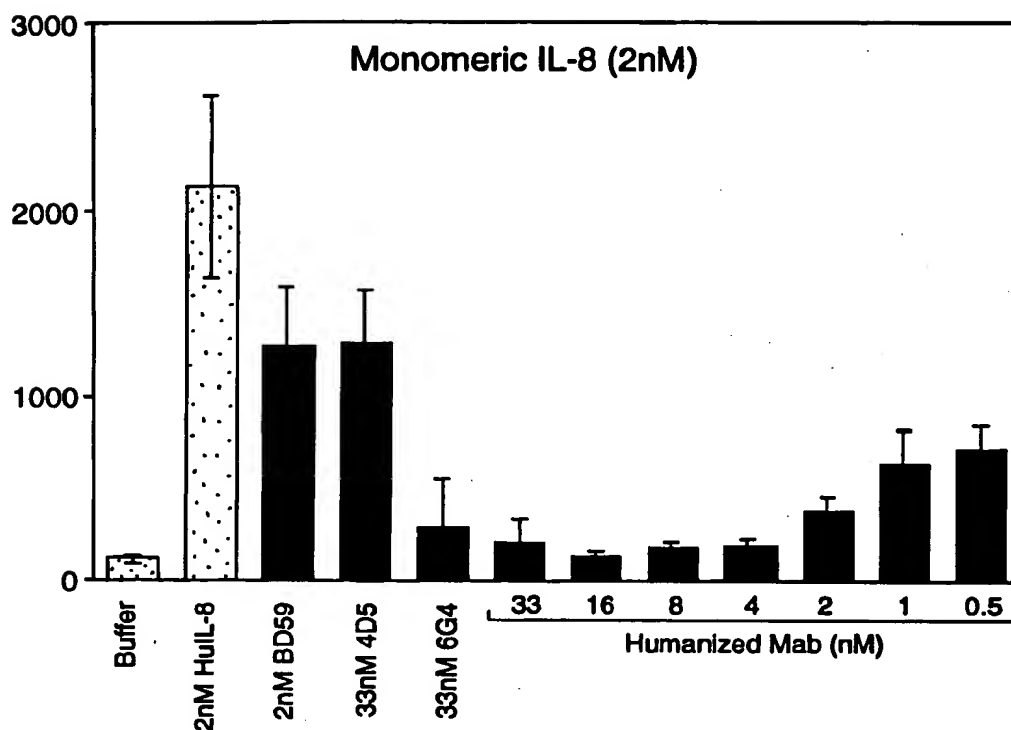


FIG. 34C

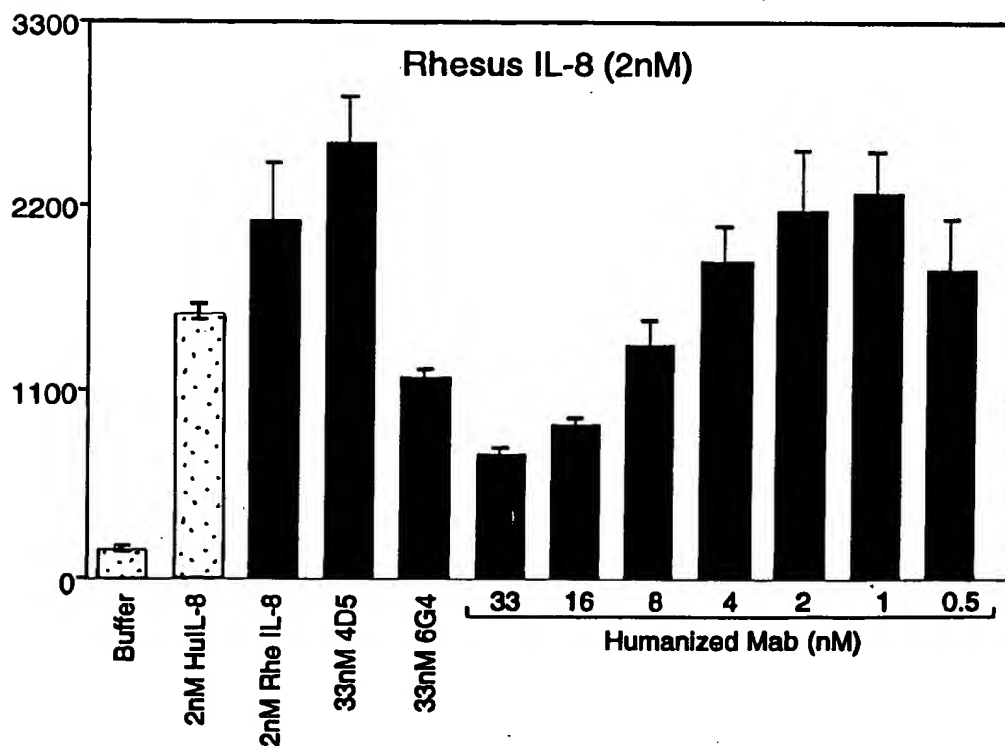


FIG. 34D



Amino Acid Sequence of the humanized anti-IL-8 6G4.2.5V11N35A Light Chain

MKKNIAFLLASMFVFSIATNAYADIQMTQSPSSLSASVGDRTTITCRSSQSLVHGIGATY
LHWYQQKPGKAPKLLIYKVSNRFSGVPSRFSGSGGTDFTLTISSLQPEDFATYYCSQST
HVPLTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDN
ALQSGNSQESVTEQDSKDSYSTLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG
EC

Amino Acid Sequence of the humanized anti-IL-8 6G4.2.5V11N35A Heavy Chain

MKKNIAFLLASMFVFSIATNAYAEVQLVQSGGGLVQPGGSLRLSCAASGYSFSSHYMH
WVRQAPGKGLEWVGYYIDPSNGETTYNQKFGRFTLSRDNSKNTAYLQMNSLRAEDTAVYY
CARGDYRYNGDWFFDVWGQGTLLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHRKPSNTK
VDKKVEPKSCDKTHT

Amino Acid Sequence of the putative Pepsin Cleavage Site and GCN4 Leucine Zipper

CPPCPAPELLGGRMKQLEDKVEELLSKNYHLENEVARLKKLVGER

FIG. 35



1 ATGAAAAAGA ATATCGCATT TCTTCTTGCA TCTATGTTTCG TTTTCTCTAT TGCTACAAAC
TACTTTTCT TATAGCGTAA AGAAGAACGT AGATACAAGC AAAAAAGATA ACGATGTTTG
-23 M K K N I A F L L A S M F V F S I A T N

61 GCATACGCTG ATATCCAGAT GACCCAGTCC CCGAGCTCCC TGTCCGCCTC TGTGGGCGAT
CGTATGCGAC TATAGGTCTA CTGGGTGAGG GGCTCGAGGG ACAGGCGGAG ACACCCGCTA
-3 A Y A D I Q M T Q S P S S L S A S V G D

121 AGGGTCACCA TCACCTGCAG GTCAAGTCAA AGCTTAGTAC ATGGTATAGG TGCTACGTAT
TCCCAGTGGT AGTGGACGTC CAGTTCAGTT TCGAATCATG TACCATATCC ACGATGCATA
18 R V T I T C R S S O S L V H G I G A T Y

181 TTACACTGGT ATCAACAGAA ACCAGGAAAA GCTCCGAAAC TACTGATTTA CAAAGTATCC
AATGTGACCA TAGTTGTCTT TGGTCCTTTT CGAGGCTTTG ATGACTAAAT GTTTCATAGG
38 L H W Y Q Q K P G K A P K L L I Y K V S

241 AATCGATTCT CTGGAGTCCC TTCTCGCTTC TCTGGATCCG GTTCTGGGAC GGATTTCACT
TTAGCTAAGA GACCTCAGGG AAGAGCGAAG AGACCTAGGC CAAGACCCTG CCTAAAGTGA
58 N R F S G V P S R F S G S G S G T D F T

301 CTGACCATCA GCAGTCTGCA GCCAGAAGAC TTCGCAACTT ATTACTGTTT ACAGAGTACT
GACTGGTAGT CGTCAGACGT CGGTCTTCTG AAGCGTTGAA TAATGACAAG TGTCTCATGA
78 L T I S S L Q P E D F A T Y Y C S O S T

361 CATGTCCCGC TCACGTTTGG ACAGGGTACC AAGGTGGAGA TCAAACGAAC TGTGGCTGCA
GTACAGGGCG AGTGCAAACC TGTCCCATGG TTCCACCTCT AGTTTGCTTG ACACCGACGT
98 H V P L T F G Q G T K V E I K R T V A A

421 CCATCTGTCT TCATCTTCCC GCCATCTGAT GAGCAGTTGA AATCTGGAAC TGCTTCTGTT
GGTAGACAGA AGTAGAAGGG CGGTAGACTA CTCGTCAACT TTAGACCTTG ACGAAGACAA
118 P S V F I F P P S D E Q L K S G T A S V

481 GTGTGCCTGC TGAATAACTT CTATCCAGA GAGGCCAAAG TACAGTGGA GGTGGATAAC
CACACGGACG ACTTATTGAA GATAGGGTCT CTCCGGTTTC ATGTCACCTT CCACCTATTG
138 V C L L N N F Y P R E A K V Q W K V D N

541 GCCCTCCAAT CGGGTAACTC CCAGGAGAGT GTCACAGAGC AGGACAGCAA GGACAGCACC
CGGGAGGTTA GCCCATTGAG GGTCTCTCA CAGTGTCTCG TCCTGTCGTT CCTGTCGTGG
158 A L Q S G N S Q E S V T E Q D S K D S T

601 TACAGCCTCA GCAGCACCTT GACGCTGAGC AAAGCAGACT ACGAGAAACA CAAAGTCTAC
ATGTCGGAGT CGTCGTGGGA CTGCGACTCG TTTCGTCTGA TGCTCTTTGT GTTTCAGATG
178 Y S L S S T L T L S K A D Y E K H K V Y

661 GCCTGCGAAG TCACCCATCA GGGCCTGAGC TCGCCCGTCA CAAAGAGCTT CAACAGGGGA
CGGACGCTTC AGTGGGTAGT CCCGACTCG AGCGGGCAGT GTTCTCTGAA GTTGTCCCCT
198 A C E V T H Q G L S S P V T K S F N R G

721 GAGTGTTAAG CTGATCCTCT ACGCCGGACG CATCGTGGCC CTAGTACGCA ACTAGTCGTA
CTCACAATTC GACTAGGAGA TGCGGCTGCG GTAGCACCGG GATCATGCGT TGATCAGCAT
218 E C O

FIG. 36



781 AAAAGGGTAT CTAGAGGTTG AGGTGATTTT ATGAAAAAGA ATATCGCATT TCTTCTTGCA
TTTTCCCATA GATCTCCAAC TCCACTAAAA TACTTTTCT TATAGCGTAA AGAAGAACGT
-1 M K K N I A F L L A

841 TCTATGTTTCG TTTTCTCTAT TGCTACAAAC GCGTACGCTG AGGTTTCAGCT AGTGCAGTCT
AGATACAAGC AAAAAAGATA ACGATGTTTG CGCATGCGAC TCCAAGTCGA TCACGTCAGA
-11 S M F V F S I A T N A Y A E V Q L V Q S

901 GCGGTGGCC TGGTGCAGCC AGGGGGCTCA CTCCGTTTGT CCTGTGCAGC TTCTGGCTAC
CCGCCACCGG ACCACGTCGG TCCCCGAGT GAGGCAAACA GGACACGTCG AAGACCGATG
8 G G G L V Q P G G S L R L S C A A S G Y

961 TCCTTCTCGA GTCATATAT GCACTGGGTC CGTCAGGCCC CGGGTAAGGG CCTGGAATGG
AGGAAGAGCT CAGTGATATA CGTGACCCAG GCAGTCCGGG GCCCATTCCC GGACCTTACC
28 S F S S H Y M H W V R Q A P G K G L E W

1021 GTTGGATATA TTGATCCTTC CAATGGTGAA ACTACGTATA ATCAAAAGTT CAAGGGCCGT
CAACCTATAT AACTAGGAAG GTTACCACTT TGATGCATAT TAGTTTTCAA GTTCCCGGCA
48 V G Y I D P S N G E T T Y N O K F K G R

1081 TTCACTTTAT CTCGCGACAA CTCCAAAAAC ACAGCATACC TGCAGATGAA CAGCCTGCGT
AAGTGAAATA GAGCGCTGTT GAGGTTTTTG TGTCGTATGG ACGTCTACTT GTCGGACGCA
68 F T L S R D N S K N T A Y L Q M N S L R

1141 GCTGAGGACA CTGCCGTCTA TTACTGTGCA AGAGGGGATT ATCGCTACAA TGGTGACTGG
CGACTCCTGT GACGGCAGAT AATGACACGT TCTCCCCTAA TAGCGATGTT ACCACTGACC
88 A E D T A V Y Y C A R G D Y R Y N G D W

1201 TTCTTCGACG TCTGGGGTCA AGGAACCCTG GTCACCGTCT CCTCGGCCCTC CACCAAGGGC
AAGAAGCTGC AGACCCAGT TCCTTGGGAC CAGTGGCAGA GGAGCCGGAG GTGGTTCCCG
108 F F D V W G Q G T L V T V S S A S T K G

1261 CCATCGGTCT TCCCCCTGGC ACCCTCCTCC AAGAGCACCT CTGGGGGCAC AGCGGCCCTG
GGTAGCCAGA AGGGGGACCG TGGGAGGAGG TTCTCGTGGA GACCCCGTG TCGCCGGGAC
128 P S V F P L A P S S K S T S G G T A A L

1321 GGCTGCCTGG TCAAGGACTA CTTCCCCGAA CCGGTGACGG TGTCGTGGAA CTCAGGCGCC
CCGACGGACC AGTTCCTGAT GAAGGGGCTT GGCCACTGCC ACAGCACCTT GAGTCCGCGG
148 G C L V K D Y F P E P V T V S W N S G A

1381 CTGACCAGCG GCGTGCACAC CTTCCCGGCT GTCCTACAGT CCTCAGGACT CTACTCCCTC
GACTGGTTCG CGCACGTGTG GAAGGGCCGA CAGGATGTCA GGAGTCCTGA GATGAGGGAG
168 L T S G V H T F P A V L Q S S G L Y S L

1441 AGCAGCGTGG TGACCGTGCC CTCCAGCAGC TTGGGCACCC AGACCTACAT CTGCAACGTG
TCGTGCGACC ACTGGCACGG GAGGTCGTG AACCCGTGGG TCTGGATGTA GACGTTGCAC
188 S S V V T V P S S S L G T Q T Y I C N V

1501 AATCACAAGC CCAGCAACAC CAAGGTGCAG AAGAAAGTTG AGCCCAAATC TTGTGACAAA
TTAGTGTTCG GGTCGTTGTG GTTCCAGCTG TTCTTTCAAC TCGGGTTTAG AACACTGTTT
208 N H K P S N T K V D K K V E P K S C D K

1561 ACTCACACAT GCGCGCCGTG CCCAGCACCA GAACTGCTGG GCGGCCGCAT GAAACAGCTA
TGAGTGTGTA CGGGCGGCAC GGGTCGTGGT CTTGACGACC CGCCGGCGTA CTTTGTGAT
228 T H T C P P C P A P E L L G G R M K Q L

FIG. 37A



1621 GAGGACAAGG TCGAAGAGCT ACTCTCCAAG AACTACCACC TAGAGAATGA AGTGGCAAGA
CTCCTGTTCC AGCTTCTCGA TGAGAGGTTC TTGATGGTGG ATCTCTTACT TCACCGTTCT
248 E D K V E E L L S K N Y H L E N E V A R

1681 CTCAAAAAGC TTGTCGGGGA GCGCTAA
GAGTTTTTCG AACAGCCCCT CGCGATT
268 L K K L V G E R O

FIG. 37B

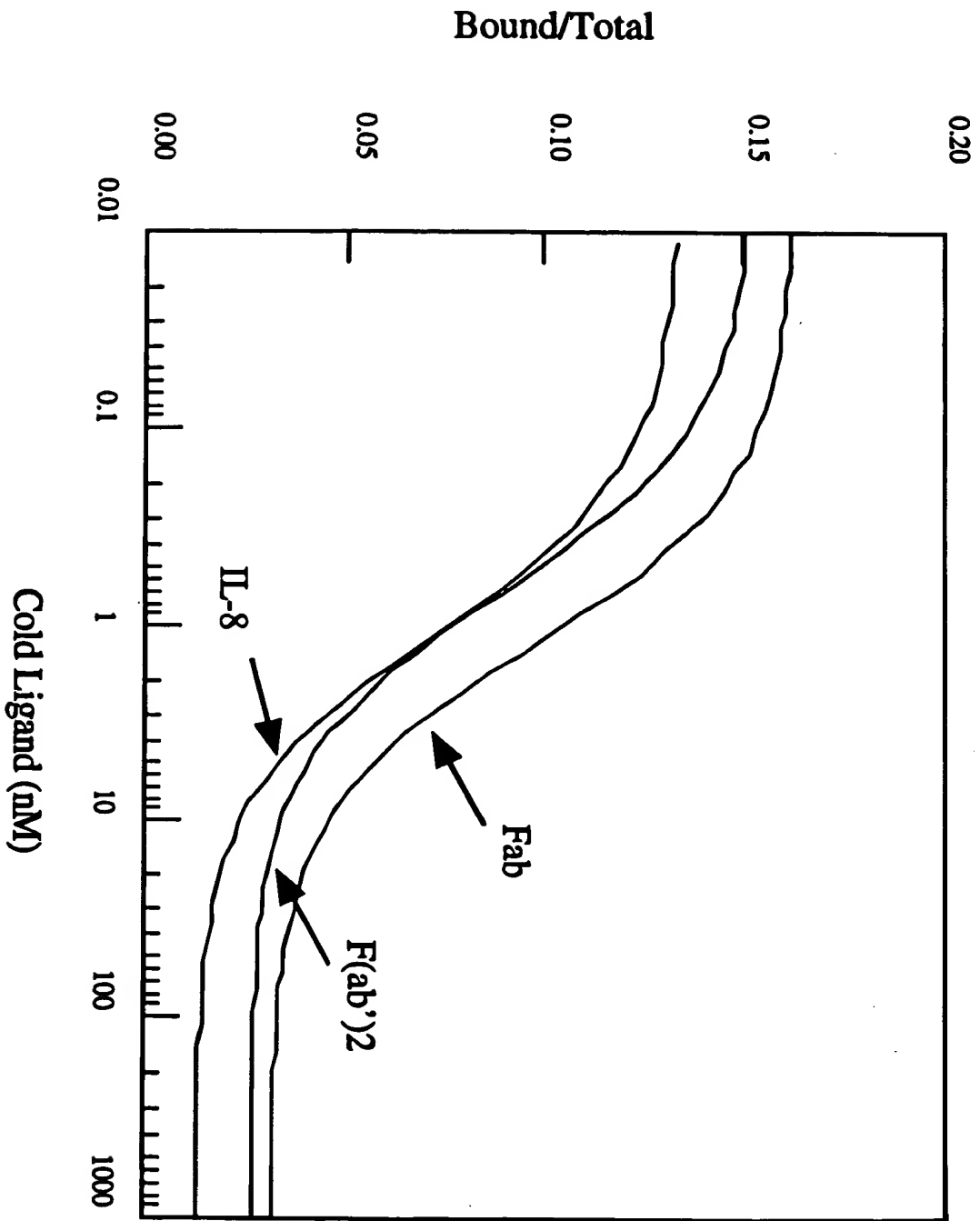


FIG. 38

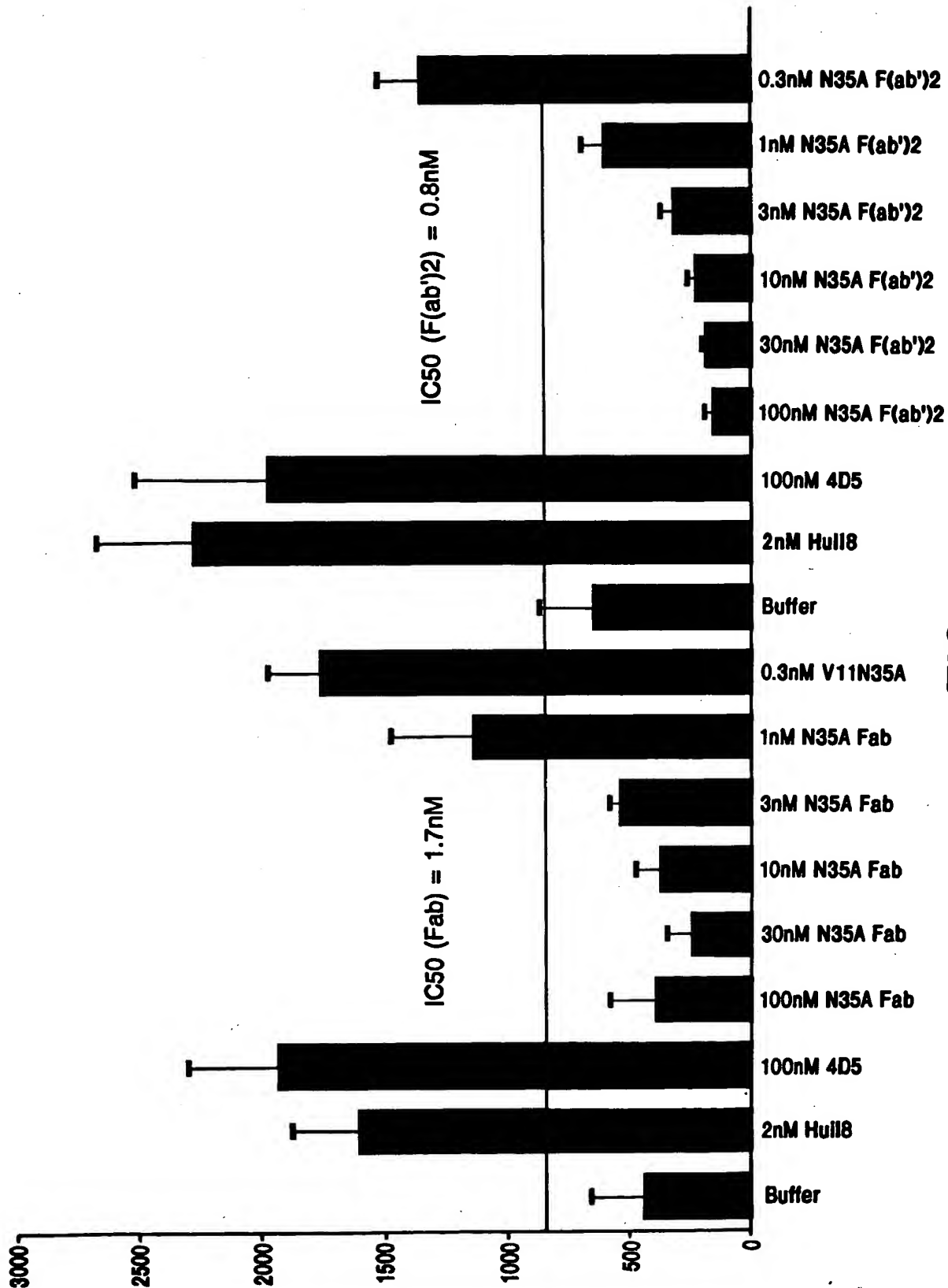


FIG. 39

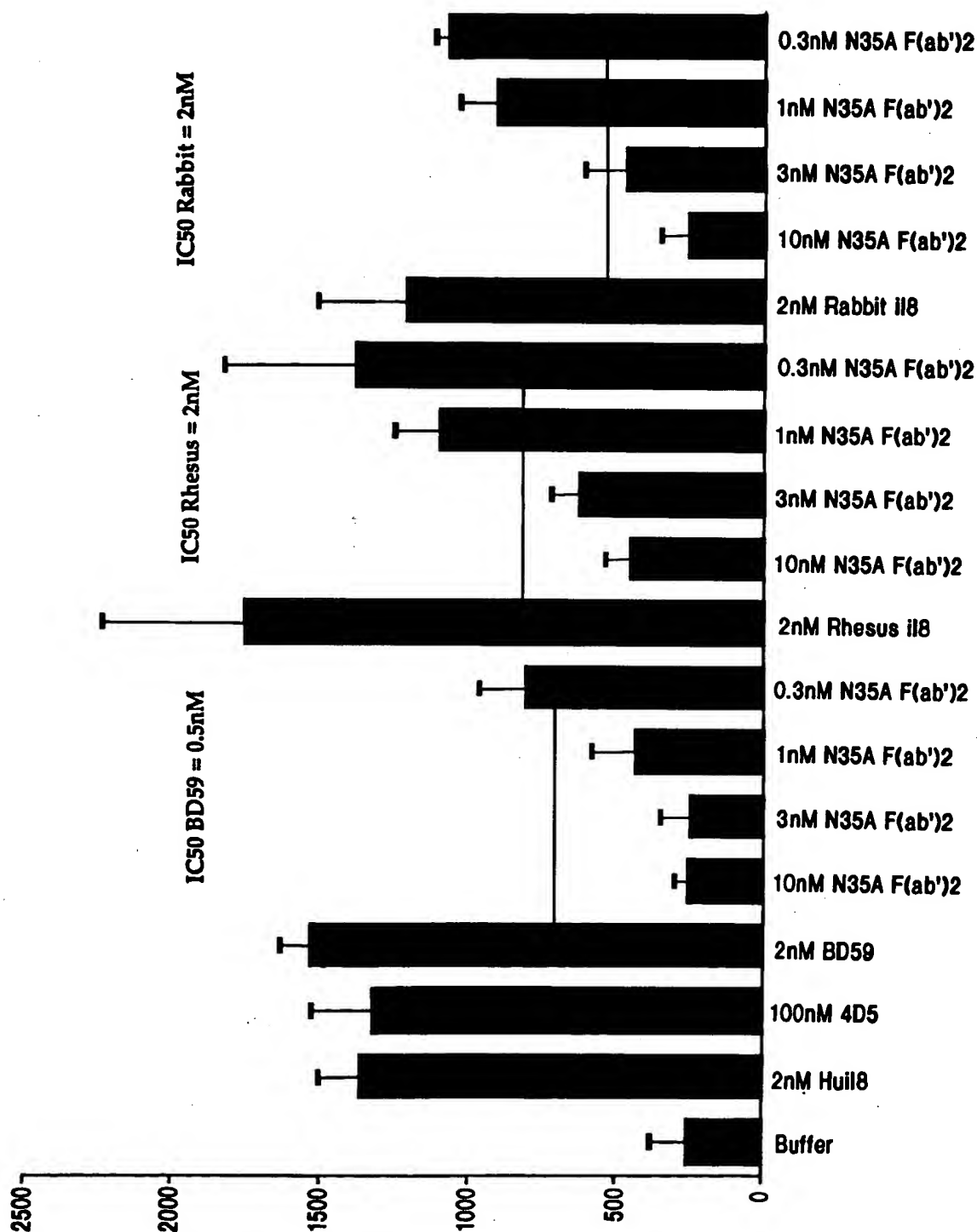


FIG. 40

FIG. 41A



```

scrFI
ncII
mspI
hpaII
dsav
xmaI/pspAI
smaI
scrFI
ncII
dsav
cauII
bsaJI
          xhoI
          mnlI
          sau3AI taqI
          mboI/ndeII[dam-]
          rsaI
          csp6I
          nlaIV nlaIV paer7I
          kpnI cauII dpuII[dam-]
          hgiCI bstYI/xhoII
          bani bsaJI alwI[dam-]
          asp718 bamHI avai
          acc65I alwI[dam-] mnlI mnlI
          401 TCGGTACCG GGGATCCTCT CGAGGTGAG GTGATTTTAT GAAAAGAAT ATCGCATTTTCTCTGCAATC TATGTTTCGTT TTTTCTATTG CTACAAACGC
          AGCCATGGGC CCTAGGAGA GTCCAACCTC CACTAAATA CTTTTCTTA TAGCGTAAG AGAACGCTAG ATACAAGCAA AAGAGATAAC GATGTTGCG
          M K K N I A F L L A S M F V F S I A T N A
          a mutation was found that inactivated the mluI site. The penultimate nucleotide was changed fr G toT ^
-23

sstI
sacI
hglJII
hgIAI/aspHI
ecII36II
bsp1286
bsiHRAI
          bsmFI bmyI
          bsrI avai aluI
          mnlI
          acII
          tth111I/aspI baniI
          ecoRV
          501 ATACGCTGAT ATCCAGATGA CCCAGTCCC CGAGTCCCCTG TCCGCCTCTG TGGCGATAG GGTCAACATC ACCTGCAGCT CAAGTCAAAG CTTAGTACAT
          TATGCCACTA TAGGTACT GGTGAGGG CCGAGGGAG AGCGGGAGAC ACCCGTATC CCAGTGTAG TGGACGTCCA GTTCAGTTTC GAATCATGA
          -2 Y A D I Q M T Q S P S S L S A S V G D R V T I T C R S S Q S L V H
          bspMI
          scfI
          pstI
          hphI
          maeIII
          bstEII hphI bsgI
          sse8387I
          bspMI
          ddeI nlaIII
          aluI
          rsaI
          hindIII csp6I
          CAAGTCAAAG CTTAGTACAT
          GTTCAGTTTC GAATCATGA

```

FIG. 41B

scrFI
 mvaI
 ecorII
 dsav
 bstNI
 bsrI
 apyI[dcmt+]
 601 GGATAGGTG CTACGTATTTT ACACGTGGTAT CAACAGAAAC CAGGAAAGC TCCGAAACTA CTGATTACAA AAGTATCCAA TCGATTCTCT GGAGTCCTT
 CCATATCCAC GATGCATAAA TGTGACCATTA GTTGTCTTG GTCTTTTCG AGGCTTTGAT GACTAAATGT TCCATAGGTT AGCTAAGAGA CCTCAGGGAA
 32 G I G A T Y L H W Y Q Q K P G K A P K L L I Y K V S N R F S G V P S
 mspI
 hpaII
 bali
 bsawI
 sau3AI
 mboI/ndeII[dam-]
 dpoI[dam+]
 dpoII[dam-]
 alwI[dam-]
 nlaIV
 bstYI/xhoII
 bamHI
 alwI[dam-] bsmFI
 701 CTGCTTCTC TGGATCCGGT TCTGGGACG ATTTCACTCT GACCATCAGC AGTCTGCAGC CAGAAGACTT CGCACTTAT TACTGTTTAC AGAGTACTCA
 GAGCGAAGAG ACTTAGGCCA AGACCTGCC TAAAGTGAGA CTGCTAGTCG TCAGACGTCG GTCTTTGAA GCCTTGAATA ATGACAAGTG TCTCATGACT
 66 R F S G S G S G T D F T L T I S S L Q P E D F A T Y X C S Q S T H
 rsaI
 csp6I
 scaI nlaIII
 styI
 bsajI
 rsaI
 csp6I
 nlaIV
 kpnI
 hgiCI
 bani
 asp718
 acc65I
 maeII
 801 TGTCCCGTC ACGTTTGGAC AGGTATCCAA GGTGGAGATC AAACGAACCTG TGGCTGCACC ATCTGTCTTC ATCTCCCGC CATCTGATGA GCAGTTGAAA
 ACAGGGCGAG TGCAAACCTG TCCCATGGTT CCACCTCTAG TTTCGCTGAC ACCGACGTCG TAGACAGAAG TAGAAGGGCG GTAGACTACT CGTCAACTTT
 99 V P L T F G Q G T K V E I K R T V A A P S V F I F P P S D E Q L K
 berBI
 aciI
 bsmFI
 sau3AI
 mboI/ndeII[dam-] fnu4HI
 dpoI[dam+]
 dpoII[dam-]
 bbsI
 mboII
 bpuAI
 bbsI
 aciI
 mboII

FIG. 41C

[illegible]

FIG. 41D



1201 AGTACGCAAC TAGTCGTAAA AAGGGTATCT AGAGGTGTGAG GTGATTTTAT GAAAGAAGAT ATGCGATTTC TTCTTGCAATC TATGTTTCGT TTTTCTATTG
TCATGCGTTC ATCAGCATTT TTCCCATAGA TCTCCAATC CACTAATAA CTTTCTCTTA TAGCGTAAAG AAGAACGTAG ATACAAGCAA AAAAGATAAC
M K K N I A F L L A S M F V F S I A

-23

1301 CTACAACGC GTACGCTGAG GTTCAGCTAG TGCAGTCTG CGGTGGCTG GTGACGCCAG GGGCTCACT CCGTTTGTC TGTGACGCTT CTGGCTACTC
GATGTTTGG CATCGGACTC CAGTCGATC ACGTGACACC GCCACCGGAC CCGGCTGTC CCGGAGTGA GGCAACACAGG ACACGTGCGA GACCGATGAG
-5 T N A Y A E V Q L V Q S G G L V Q P G G S L R L S C A A S G Y S

FIG. 41E

FIG. 41E

[illegible]

FIG. 41G

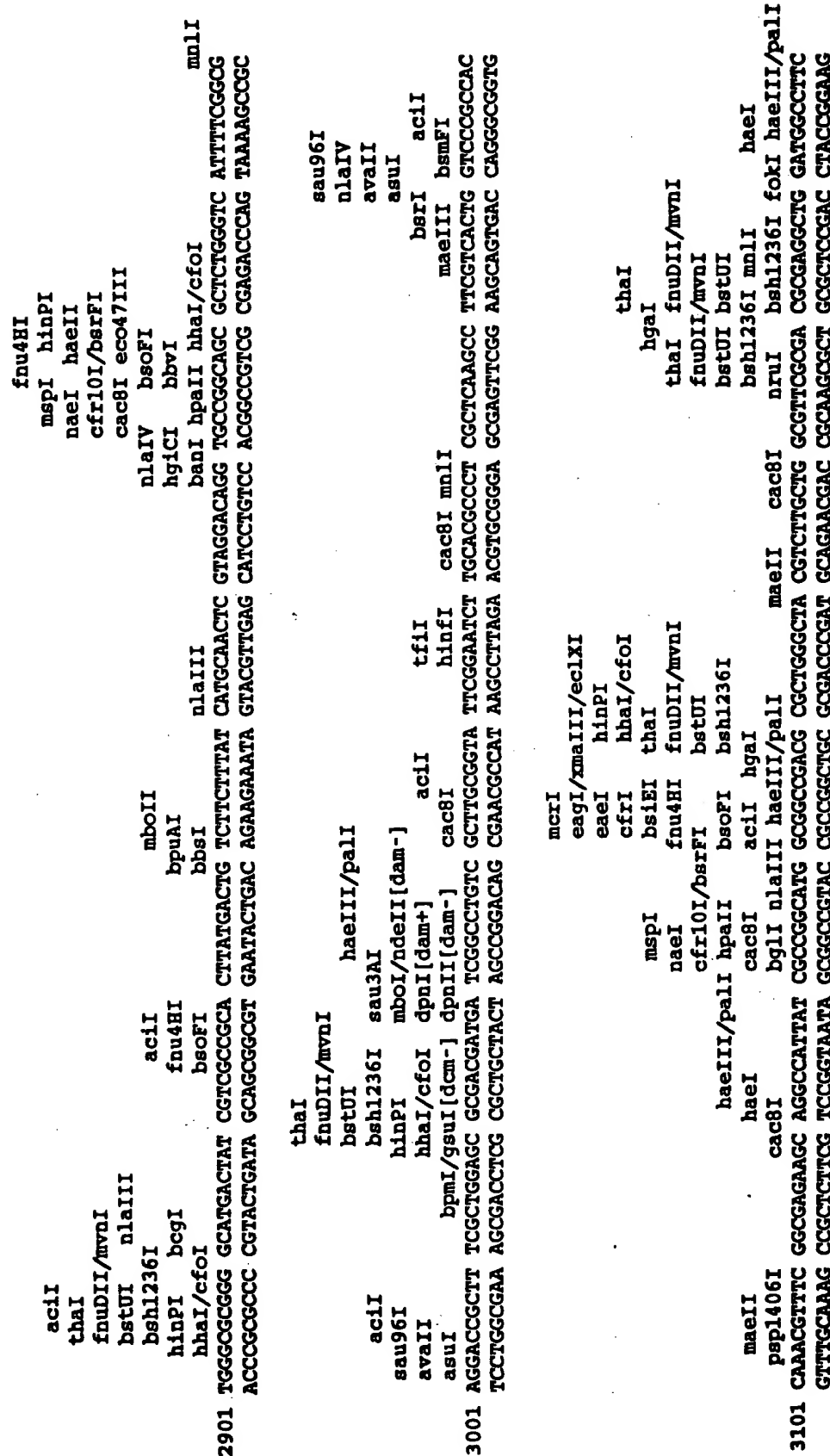
[illegible]

FIG. 41H

2301 AATGGCTCA TCGTCATCCT CGGCACCGTC ACCCTGGATG CTGTAGGCAT AGGCTTGGTT ATGCCGGTAC TGCCTGGCCT CTTCGGGGAT ATCGTCCATT
 TTACGGGAGT AGCAGTAGGA GCGGTGGCAG TGGGACCTAC GACATCCGTA TCGGAACCAA TACGGCCATG ACGGCCCGGA GAACGCCCTA TAGCAGGTAA
 2401 CCGACAGCAT CGCCAGTCACT TATGGCGTGC TGCCTAGCGCT ATATGCGTGT ATGCAATTTC TATGGCGCAC CGTTCTCGGA GCACGTGTCG ACGGCTTTCG
 GGCTGTGCTA GCGGTCACTG ATACCGCAGC ACGATCGCGA TATACGCAAC TAGCTTAAAG ATACGGCTGG GCAAGAGCCT CGTGACAGGC TGGCGAAACC
 2501 CGCGCGCCCA GTCCTGCTCG CTTGCGTACT TGGAGCCACT ATCGACTACG CGATCATGCG GACCAACCC GTCTGTGGA TCCTCTACGC CGGACGCATC
 GCGCGGGGT CAGGACGAGC ACGTGGATGA ACCTCGGTGA TACTGTATGC GCTAGTACCG CTGCTGTGGC CAGGACACCT AGGAGATGCG GCCTGGGTAG

FIG. 41I

FIG. 41J





3201 CCCATTATGA TTCTTCTCGC TTCCGGCGGC ATCGGGATGC CCGCGTTGCA GGCCATGCTG TCCAGGCAGG TAGATGACGA CCATCAGGGA CAGCTTCAAG
GGTAATACT AAGAAGAGCG RAGGCCGCGG TAGCCCTACG GGCGCAACGT CCGGTACGAC AGTCCGTCC ATCTACTGCT GGTAGTCCCT GTCGAAGTTC
bspMI
thai
fnu4HI
bsOFI
acII
mboII
tfII
hinFI
3301

3301 GATCGCTCGC GGCTCTTACC AGCCTAATCG TCGGATTGAA GCTAGTGACC TGGCGACTAG CAGTCCGCTG AAATACGGCG GAGCCGCTCG TGTACTTGC CCAACCGTAC
CTACGAGCG CCGAGAATGG
fnu4HI
bsOFI
acII
thai
fnuDII/mvni
bstUI
cac8I
sau3AI
mboI/ndeII[dam-]
dpnI[dam+]
dpnII[dam-]
taqI[dam-]
3401
GATCGCTCGC
CTACGAGCG
CGGCTCTTACC
AGCCTAATCG
TCGGATTGAA
GCTAGTGACC
TGGCGACTAG
CAGTCCGCTG
AAATACGGCG
GAGCCGCTCG
TGTACTTGC
CCAACCGTAC

3401 GATTGTAGC GCCGCCCTAT ACCTTGCTCG CTCTCCCGCG TTGCGTCCG GTGCATGGAG CCGGCCACCG TCGACCTGAA TGGAGCCCG CGGCACCTCG
CTACATCCG CCGCGGGATA TGGACACGAC GGAGGGGCGC AACGCGGCGC CACGTACCTC GGCCCGGTGG AGCTGGACTT ACCTTCGGCC GCGGTGGAGC
fnu4HI
bsOFI
hinPI
hbaI/cfoI
nlaIV
nari
kasi
hinII/acyI
hgiCI
haeII
bani acII
abaiI/bsaHI
3401
GATTGTAGC
GCCGCCCTAT
ACCTTGCTCG
CTCTCCCGCG
TTGCGTCCG
GTGCATGGAG
CCGGCCACCG
TCGACCTGAA
TGGAGCCCG
CGGCACCTCG
CTACATCCG
CGGCTCTTACC
AGCCTAATCG
TCGGATTGAA
GCTAGTGACC
TGGCGACTAG
CAGTCCGCTG
AAATACGGCG
GAGCCGCTCG
TGTACTTGC
CCAACCGTAC

FIG. 41L

[illegible]

FIG. 41M



```

sau3AI
mboI/ndeII{dam-}
nani{dam-}
dpuI{dam+}
dpuII{dam-}
bstYI/xhoII
alwI{dam-}
mspI
hpaiI
mroI bsaBI{dam-} fnu4HI
bspMI
bspEI{dam-} bsoFI
bsaWI sfaNI bsvI
accIII{dam-} sfaNI
foki cac8I
3801 TGGTCTTCGG TTTCCTGCTT TCGTAAAGTC TGGAAACGG GAAGTCAGCG CCTGCAACA TTATGTTCCG GATCTGCATC GCAGGATGCT GCTGGCTACC
ACCAAGAGCC AAAGGCACAA AGCATTTTCAG ACCTTTGGC CTTCACTGCG GGAAGCTGCT AATACAAAGC CTAGACGTAG CTTCTTACGA CGACCGATGG
acII
thai
fnuDII/mvuI hinPI
bstUI hhai/cfoI
bsh1236I haeII mslI
3901 CTGTGGAACA CCTACATCTG TATTACGAA CGGCTGGCAT TGACCCTGAG TGATTTTCT CTGGTCCGC CGCATCCATA CCGCCAGTTG TTTACCCCTCA
GACACCTTGT GGATGTAGAC ATAATTGCTT CGCGACCGTA ACTGGGACTC ACTAAAAGA GACCAGGGCG GCTAGGTAT GCGGTCAAC AAATGGGAGT
cac8I
hinPI
hhai/cfoI
tru9I haeII
mseI eco47III
ddeI
acII
bmfI foki
sau96I sfaNI
nlaIV acII
avaII fnu4HI bsrI
asuI bsoFI acII mnlI
3901 CTGTGGAACA CCTACATCTG TATTACGAA CGGCTGGCAT TGACCCTGAG TGATTTTCT CTGGTCCGC CGCATCCATA CCGCCAGTTG TTTACCCCTCA
GACACCTTGT GGATGTAGAC ATAATTGCTT CGCGACCGTA ACTGGGACTC ACTAAAAGA GACCAGGGCG GCTAGGTAT GCGGTCAAC AAATGGGAGT
nspl
scrFI
ncII
mspl
bsrI hpaiI
bsII dsav nlaIII
maeII caulI
maeIII nspHI
4001 CAACGTTCCA GTAACCGGC ATGTTTCATCA TCAGTAACCC GTATCGTGAG CATCTCTCT CGTTTCATCG GTATCATTAC CCCATGAAC AGAATTTCCC
GTTCGAAGGT CATGGCCG TACAAGTAGT AGTCATTGGG CATAGCACTC GTAGGAGAGA GCMACTAGC CATAGTAATG GGGTACTTG TCTTTAAGG
nlaIII apoI belI
```

FIG. 41N



hgiAI/aspHI
 bsp1286
 bsiHKA1
 bmyI ndeI
 apaLI/snoI
 alw44I/snoI
 ddel
 rsaI
 csp6I
 GATGTACTG AGAGTGCACC
 CTATCATGAC TCTCACGTGG
 4401 CGGGTGTCCG GCGCAGCCA TGACCCAGTC ACGTAGCGAT AGCGGAGTGT ATACTGGCTT AACTATGCGG CATCAGAGCA
 4501 ATATGCGGTG TGAATATCCG CACAGATCCG TAAGGAGAAA ATACCGCATC AGCGGCTCTT CCGCTTCCTC GCTCACTGAC TCGCTGCGCT CGGTGCTGTCG
 TATACGCCAC ACTTATGCG GTGTCTAGCG ATTCTCTCTT TATGCGTAG TCCGCGAGMA GCGGAAGGAG CGAGTGACTG AGCGAGCGGA GCCAGCAAGC
 4601 GCTGCGCGGA CCGGTATCAG CTCACCTCAA GCGGGTAATA CCGTTATCCA CAGATCAGG GGATACGCA GGAAAGAAC TGTGAGCAAA AGGCCAGCAA
 CGACGCGCT CGCCATAGTC GAGTGAGTT CCGCCATTAT GCCAATAGGT GTCTTAGTCC CCTATTGCGT CCTTCTTGT ACACCTGTTT TCGGTGCTT
 4701 AAGGCCAGGA ACCGTAAAA GCGCGCGTGT CTGGCGTTT TCCATAGCT CCGCCCCCT GACGAGCATC ACMAAATCG ACGTCAAGT CAGAGGTGGC
 TCCGCTCT TGGCATTTT CCGCGGCMAC GACCGCAAAA AGGTATCCGA GCGCGGGGA CTGCTCGTAG TGTTTTAGC TCGGAGTCA GTCTCCACCG

FIG. 41P

scrFI

scrFI mvaI
mvaI ecorII
ecorII dsav
dsav bstNI
bstNI apyI[dcmt+] bsaJI aluI mnLI hhaI/cfoI
bsSI

bslI

acII mspl
fnu4HI hpall
bsoFI bsaWI acII

4801 GAAACCCGAC AGGACTATAA AGATACAGG CGTTTCCCCC TGGAGACTCC CTCGTGCCT CTCTGTTC GACCCTGCC CTTACCGGAT ACCTGTCCGC
CTTTGGCTG TCCTGATATT TCTATGCTCC GCNAAGGGG ACCTTCGAG GAGCACGGA GAGACAAGG CTGGGACGGC GAATGGCCTA TGGACAGGCG

hgIAI/aspHI
bsp1286
bsIHKA I
bmyI
apaLI/snoI
alw44I/snoI

4901 CTTTCTCCCT TCGGGAAGCG TGGCGCTTC TCATAGCTCA CGCTGTAGGT ATCTCAGTTC GGTTAGGTC GTTCGTCCA AGCTGGGTG TGTGCACGAA
GAAAGAGGGA AGCCCTTCG ACCGCGAAG AGTATCGAGT GCGACATCCA TAGAGTCAAG CCACATCCAG CAAGCGAGGT TCGACCCGAC ACACGTGCTT

alnWI[dcmt-]
fnu4HI
fnu4HI
bsoFI
fnu4HI
bsoFI
bbvI
bsrI bbvI bsrI
maeIII

mspl
hpall
scrFI
ncII
dsav
pleI
hinfi
cauII

5001 CCCCCCGTTC AGCCCGACCG CTGCGCCTTA TCCGGTAAT ATCGTCTTGA GTCCAACCCG GTAAGACACG ACTTATGCC ACTGGCAGCA GCCACTGGTA
GGGGGCGNAG TCGGCTCGC GACGCGGAAT AGGCCATTGA TAGCAGNACT CAGGTTGGC CATTTGTGC TGAATAGCG TGAACCTGCGT CCGTGACCAT

bslI
hmaI
mael
haeIII/pali
hael

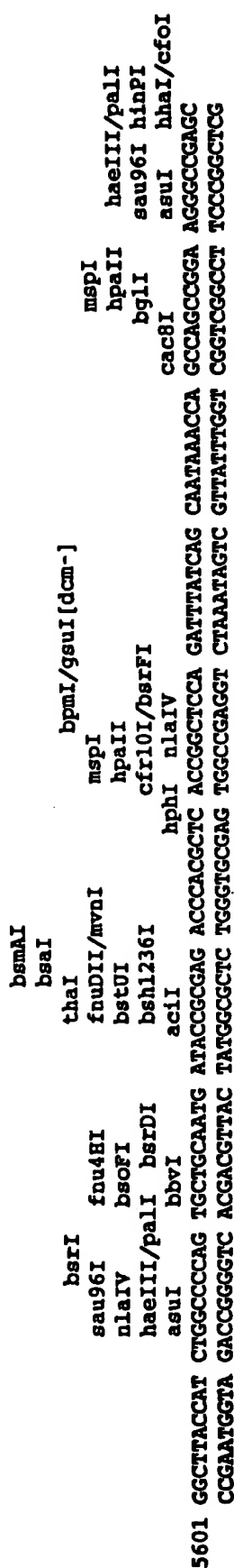
mnLI acII scfi

5101 ACAGGATTAG CAGAGCGAGG TATGTAGCG GTGCTACAGA GTTCTTGAAG TGGTGGCCTA ACTACGGCTA CACTAGAAG ACAGTATTG GTATCTGGC
TGTCCTAATC GTCTCGCTCC ATACATCCGC CACGATGTCT CAGAACTTC ACCACCGGAT TGATGCCGAT TGATCTTCC TGTATAAAC CATAGACGCG

hinPI
bhai/cfoI
bfai
bhai/cfoI

FIG. 41Q







```
mcrl  
bslEI  
bcgI  
fnu4HI  
bsOFI  
acII  
rsal  
bsrI  
scal  
maeIII hphI csp6I  
dcl  
6001 ATTCTCTTAC TGTCAAGCA TCCGTAAGAT GCTTTCTGT GACTGGTGAG TACTCAACCA AGTCATTCTG AGAATAGTGT ATGCGGCGAC CGAGTTGCTC  
TAAGAGAATG ACAGTAGCGT AGGCATTCTA CGAAAGACA CTGACCACTC ATGAGTTGGT TCAGTAAGAC TCTTATCACA TACGCGCTG GCTCAACGAG  
hgaI  
hnlI/acyI  
ahaiI/bsaHI  
mspI  
hpaII  
scrFI  
ncII  
dsav  
cauII hincII/hindII  
acII  
hlnPI  
hhaI/cfoI  
thaI  
fnuDII/mvni  
bstUI  
bsh1236I  
bsrI  
taqI  
sau3AI  
mboI/ndeII[dam-]  
dpnI[dam+]  
dpnII[dam-]  
bstYI/xhoII  
alwI[dam-]  
nspBII  
acII  
bstYI/xhoII  
maeIII  
bssSI  
alw44I/snoI  
dpnI[dam+]  
dpnII[dam-]  
hphI  
6201 TTACCGCTGT TGAGATCCAG TTCGATGTAA CCCACTCTGT CACCCAACTG ATCTTCAGCA TCTTTTACTT TCACCAGCGT TTCTGGGTGA GCAAAAACAG  
AATGGCGACA ACTCTAGGTC AAGCTACATT GGGTGAGCAC GTGGGTGAC TAGAAGTGT AGAAATGAA AGTGCTGCA AAGACCCACT CGTTTTTGTC  
acII  
fnu4HI  
bsOFI  
msII  
earI/ksp632I  
sapi  
mboII  
6301 GAAGGCAAAA TGCCGCAAAA AAGGGAATAA GGGCGACAG GAAATGTGA ATACTCATAC TCTTCTTTT TCAATATTAT TGAAGCATTT ATCAGGGTTA  
CTCCGTTTT ACGGCGTTTT TTCCCTTATT CCGCTGTGC CTTTACAAC TATGAGTAG AGAAGGAAA AGTTATAATA ACTTCGTAAA TAGTCCCAAT
```

FIG. 41T



hlnPI
 thal
 fndDII/mvnI
 bstUI
 bsh1236I
 acil
 nlaIV hbaI/cfoI
 bsmAI bspHI
 nlaIII
 rcaI
 bspHI acil
 bsmAI bspHI
 6401 TTGTCTCATG AGCGGATACA TATTGTAAG TATTAGAAA ATAAACAAA TAGGGTTC GCGACATTT CCGCGAAAAG TGCCACCTGA CGTCTAAGAA
 AACAGAGTAC TCGCCTATGT ATAAACTTAC ATAAATCTTT TTATTGTTT ATCCCCAAG CGGTGTAAA GGGGCTTTTC ACGGTGGACT GCAGATTCTT
 sau96I
 haeIII/palI
 asuI mboII
 ecoO109I/draII
 mnlI bpuAI
 bssSI bbsI
 nlaIII
 rcaI tru9I
 bspHI msel
 6501 ACCATTATTA TCATGACATT AACCTATAAA ATAGGCGTA TCACGAGGCC CTTTCGTCTT CAA
 TGGTAATAAT AGTACTGTAA TTGGATATTT TTATCCGCAT AGTGTCCGG GAAAGCAGAA GTT

FIG. 41U



>length: 6563

aatII(GACGTC):	1645 6489
acc65I(GGTACC):	403 823
accI(GTAKAC):	1093 1963 4449
accII(TCCGGA):	3867[dam-]
acII(CCGC):	178 542 805 877 1340 1750 1826 2011 2039 2043 2182 2242 2384 2492 2501 2504
	2628 2781 2784 2787 2906 2926 3005 3045 3094 3141 3226 3241 3309 3342 3367 3412
	3436 3448 3490 3544 3597 3613 3619 3700 3838 3967 3970 3981 4139 4155 4210 4266
	4351 4390 4400 4442 4467 4505 4518 4544 4561 4604 4611 4632 4723 4751 4878 4897
	5018 5128 5263 5272 5634 5725 5916 5962 6083 6127 6204 6313 6412 6459
acyI	see hinII
aflIII(ACRYGT):	1307 4678
ageI(ACOGT):	1788
ahaII/baaII(GRCGYC):	1645 1813 2616 2637 2751 3408 6107 6489
ahaII/draI(TTTAAA):	5435 5454 6146
ahdI/eamI105I(GACNNNNNGTC):	346 5566
aluI(AGCT):	72 121 252 320 398 532 589 648 1126 1144 1167 1325 1386 1906 2054 2075 2126
	2218 2233 2889 3292 4202 4259 4270 4319 4338 4619 4845 4935 4981 5238 5759 5859
	5922
alw44I/snoI(GTGCAC):	1831 4494 4992 6238
alwI[dam-](GGATC):	412 413 712 713 1171 1471 2578 2579 3300 3870 5245 5319 5331 5416 5429 5893
	6196 6214
alwNI[dcn-](CAGNNNCTG):	1117 1385 5089
apaI(GGGCCC):	1695
apaLI/snoI(GTGCAC):	1831 4494 4992 6238
apoI(RAATY):	1 391 4093
apyI[dcn+](CCWGG):	640 999 1347 1357 1449 1665 1713 1755 1764 2333 3262 3645 4705 4826 4839
aseI/asnI/aspI(ATAAT):	5742
asnI	see aseI
asp700(GAANNNTTC):	905 930 4234 6166
asp718(GGTACC):	403 823
asphi	see hgiAI
aspi	see thIIII
asuI(GGNCC):	1119 1195 1425 1434 1446 1512 1695 1696 1752 2155 2375 2727 3002 3090 3339 3463

FIG. 41V



Stop Template Primer

SL.97.2 5' CAT GGT ATA GGT TAA ACT TAT TTA CAC 3'

NNS Randomization Primer

SL.97.3 5' CAT GGT ATA GGT NNS ACT TAT TTA CAC 3'

FIG. 42



Randomization of Position N35 of Variable Light Chain CDR-1
Amino Acid Frequency

Phage Display (NNS Codon Library) Sort #3

Amino Acid	Frequency	% Total	IC50 (nM)
Asparagine (wt)	1	5.6	4.9
Glycine	6	16.6	3.1
Aspartic Acid	3	16.6	3.1
Glutamic Acid	4	22.2	0.1
Alanine	2	5.6	0.2
Lysine	1	5.6	ND
Serine	1	1.9	ND

FIG. 43A

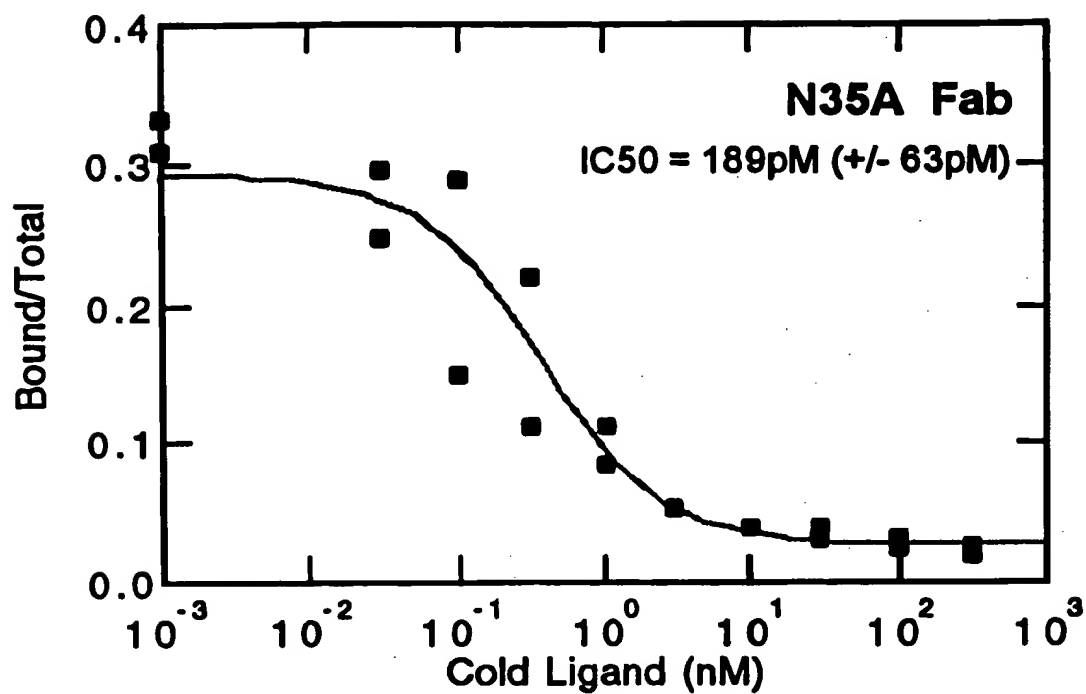


FIG. 43B-1

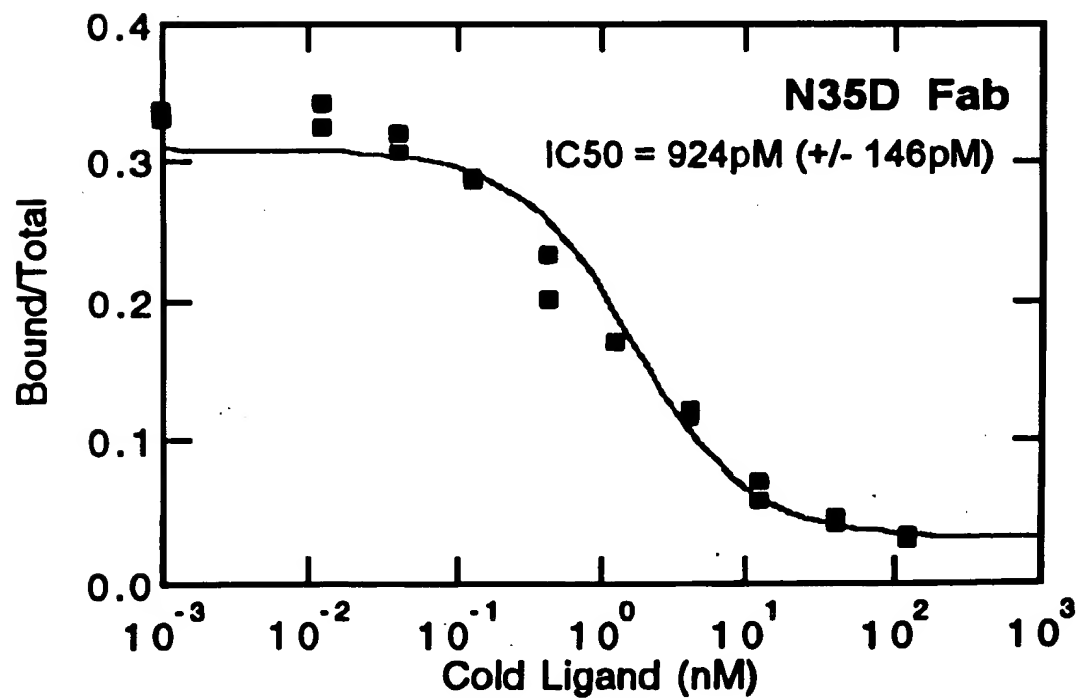


FIG. 43B-2

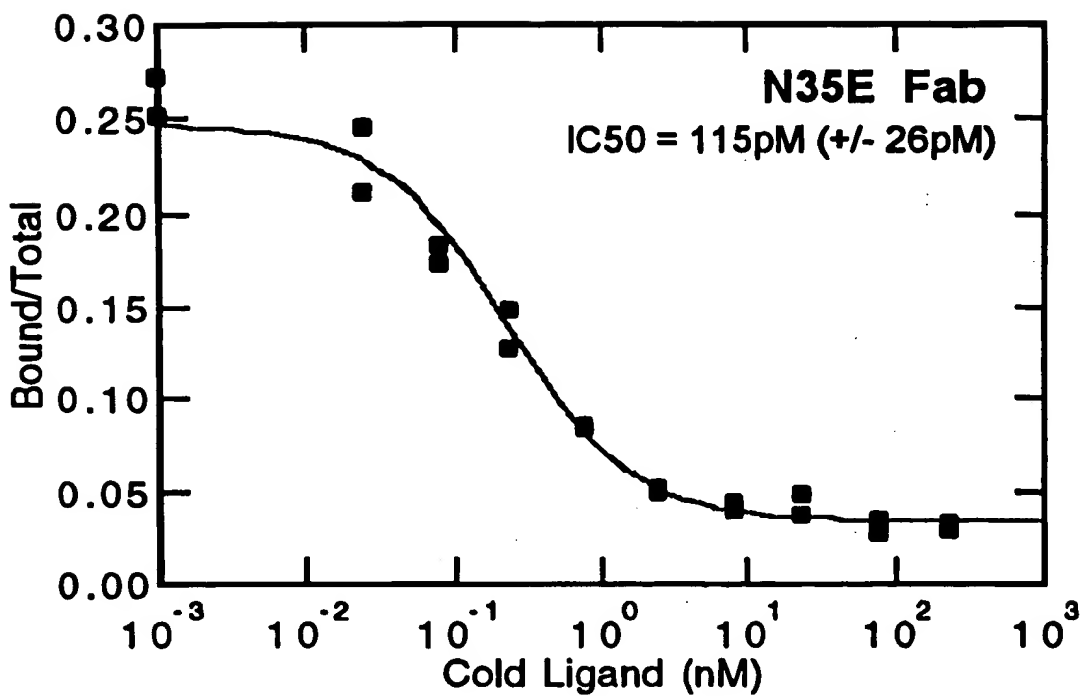


FIG. 43B-3

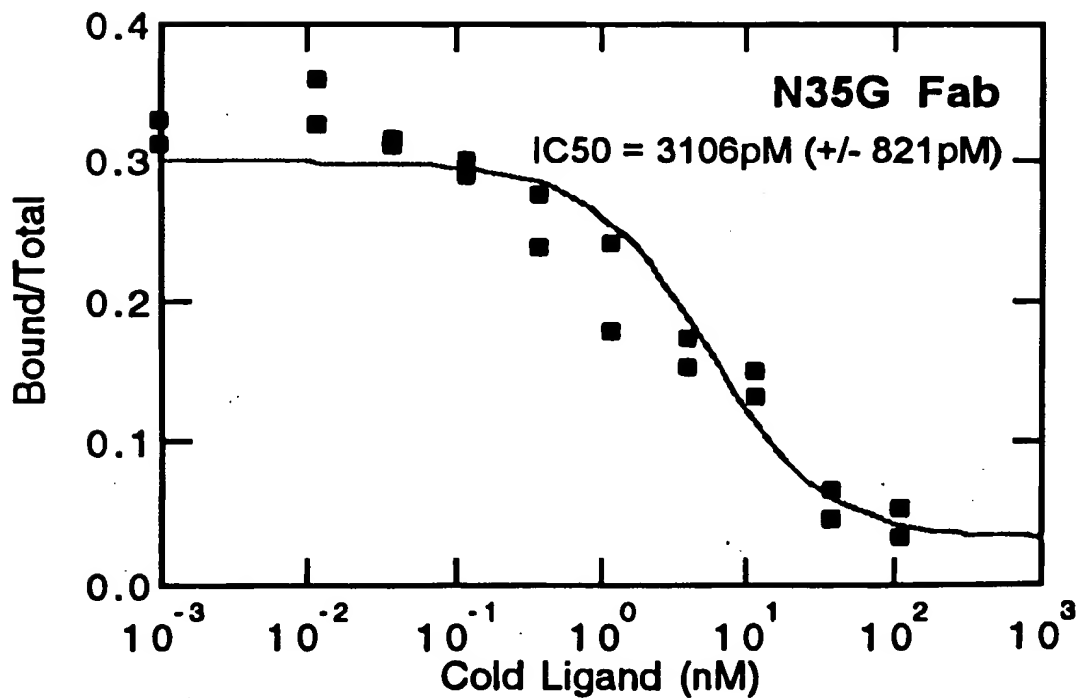
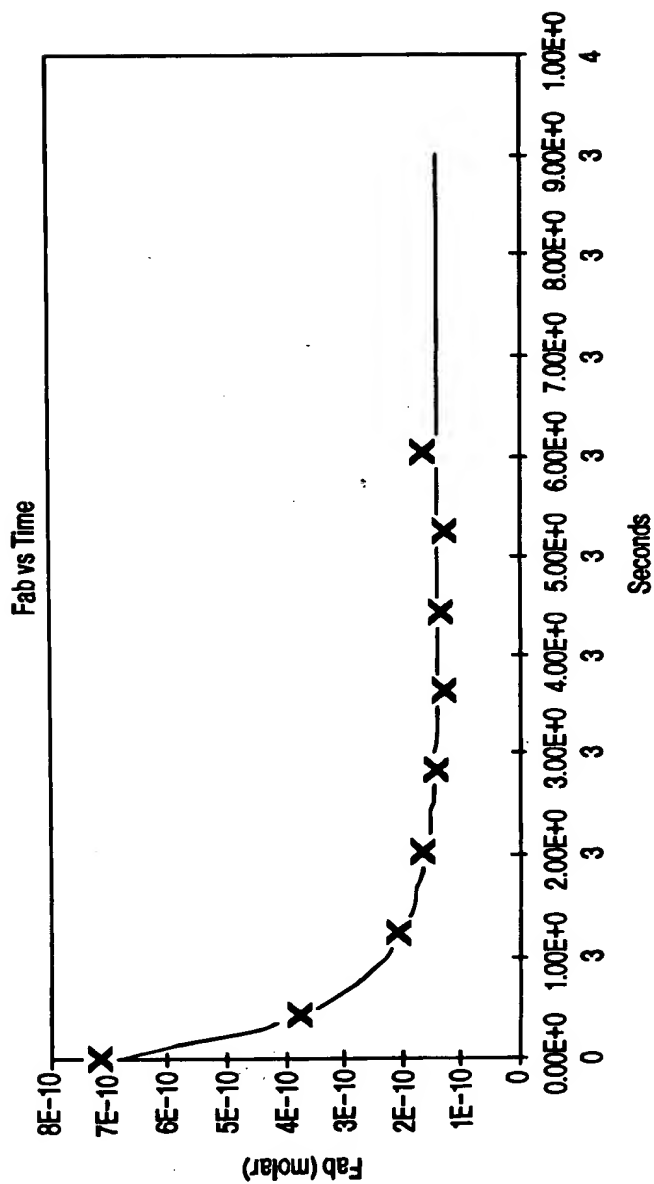


FIG. 43B-4



Representative Conc versus Time Plot. Shown is the kinetic data for 6G4V11N35A.F(ab')₂.

SAMPLE	ka	kd	Kd
6G4V11N35A-Fab	ND	ND	114pM
6G4V11N35A-F(ab') ₂	2.0x10 ⁶	2.1x10 ⁻⁴	109pM
6G4V11N35E-Fab	4.7x10 ⁶	2.6x10 ⁻⁴	54pM

FIG. 44



1 ATGAAAAAGA ATATCGCATT TCTTCTTGCA TCTATGTTCTG TTTTTCCTAT TGCTACAAAC
TACTTTTCT TATAGCGTAA AGAAGAACGT AGATACAAGC AAAAAAGATA ACGATGTTTG
-23 M K K N I A F L L A S M F V F S I A T N

61 GCATACGCTG ATATCCAGAT GACCCAGTCC CCGAGCTCCC TGTCCGCCTC TGTGGGCGAT
CGTATGCGAC TATAGGTCTA CTGGGTCAGG GGCTCGAGGG ACAGGCGGAG ACACCCGCTA
-3 A Y A D I Q M T Q S P S S L S A S V G D

121 AGGGTCACCA TCACCTGCAG GTCAAGTCAA AGCTTAGTAC ATGGTATAGG TGAGACGTAT
TCCAGTGGT AGTGGACGTC CAGTTCAGTT TCGAATCATG TACCATATCC ACTCTGCATA
18 R V T I T C R S S O S L V H G I G E T Y

181 TTACACTGGT ATCAACAGAA ACCAGGAAAA GCTCCGAAAC TACTGATTTA CAAAGTATCC
AATGTGACCA TAGTGTCTT TGGTCCTTTT CGAGGCTTTG ATGACTAAAT GTTTCATAGG
38 L H W Y Q Q K P G K A P K L L I Y K V S

241 AATCGATTCT CTGGAGTCCC TTCTCGCTTC TCTGGATCCG GTTCTGGGAC GGATTTCACT
TTAGCTAAGA GACCTCAGGG AAGAGCGAAG AGACCTAGGC CAAGACCCTG CCTAAAGTGA
58 N R F S G V P S R F S G S G S G T D F T

301 CTGACCATCA GCAGTCTGCA GCCAGAAGAC TTCGCAACTT ATTACTGTTT ACAGAGTACT
GACTGGTAGT CGTCAGACGT CGGTCTTCTG AAGCGTTGAA TAATGACAAG TGTCTCATGA
78 L T I S S L Q P E D F A T Y Y C S O S T

361 CATGTCCCGC TCACGTTTGG ACAGGGTACC AAGGTGGAGA TCAAACGAAC TGTGGCTGCA
GTACAGGGCG AGTGCAAACC TGTCCCATGG TTCCACCTCT AGTTTGCTTG ACACCGACGT
98 H V P L T F G Q G T K V E I K R T V A A

421 CCATCTGTCT TCATCTTCCC GCCATCTGAT GAGCAGTTGA AATCTGGAAC TGCTTCTGTT
GGTAGACAGA AGTAGAAGGG CGGTAGACTA CTCGTCAACT TTAGACCTTG ACGAAGACAA
118 P S V F I F P P S D E Q L K S G T A S V

481 GTGTGCCTGC TGAATAACTT CTATCCAGA GAGGCCAAAG TACAGTGGAA GGTGGATAAC
CACACGGACG ACTTATTGAA GATAGGGTCT CTCCGGTTTC ATGTCACCTT CCACCTATTG
138 V C L L N N F Y P R E A K V Q W K V D N

541 GCCCTCCAAT CGGGTAACTC CCAGGAGAGT GTCACAGAGC AGGACAGCAA GGACAGCACC
CGGGAGGTTA GCCCATTGAG GGTCTCTCA CAGTGTCTCG TCCTGTCGTT CCTGTCTGTTG
158 A L Q S G N S Q E S V T E Q D S K D S T

601 TACAGCCTCA GCAGCACCTT GACGCTGAGC AAAGCAGACT ACGAGAAACA CAAAGTCTAC
ATGTCGGAGT CGTCGTGGGA CTGCGACTCG TTTCGTCTGA TGCTCTTTGT GTTTCAGATG
178 Y S L S S T L T L S K A D Y E K H K V Y

661 GCCTGCGAAG TCACCCATCA GGGCCTGAGC TCGCCCGTCA CAAAGAGCTT CAACAGGGGA
CGGACGCTTC AGTGGGTAGT CCCGACTCG AGCGGGCAGT GTTCTCGAA GTTGTCCCCT
198 A C E V T H Q G L S S P V T K S F N R G

721 GAGTGTTAAG CTGATCCTCT ACGCCGGACG CATCGTGGCC CTAGTACGCA ACTAGTCGTA
CTCACAATTC GACTAGGAGA TCGGCCTGC GTAGCACCGG GATCATGCGT TGATCAGCAT
218 E C O

FIG. 45

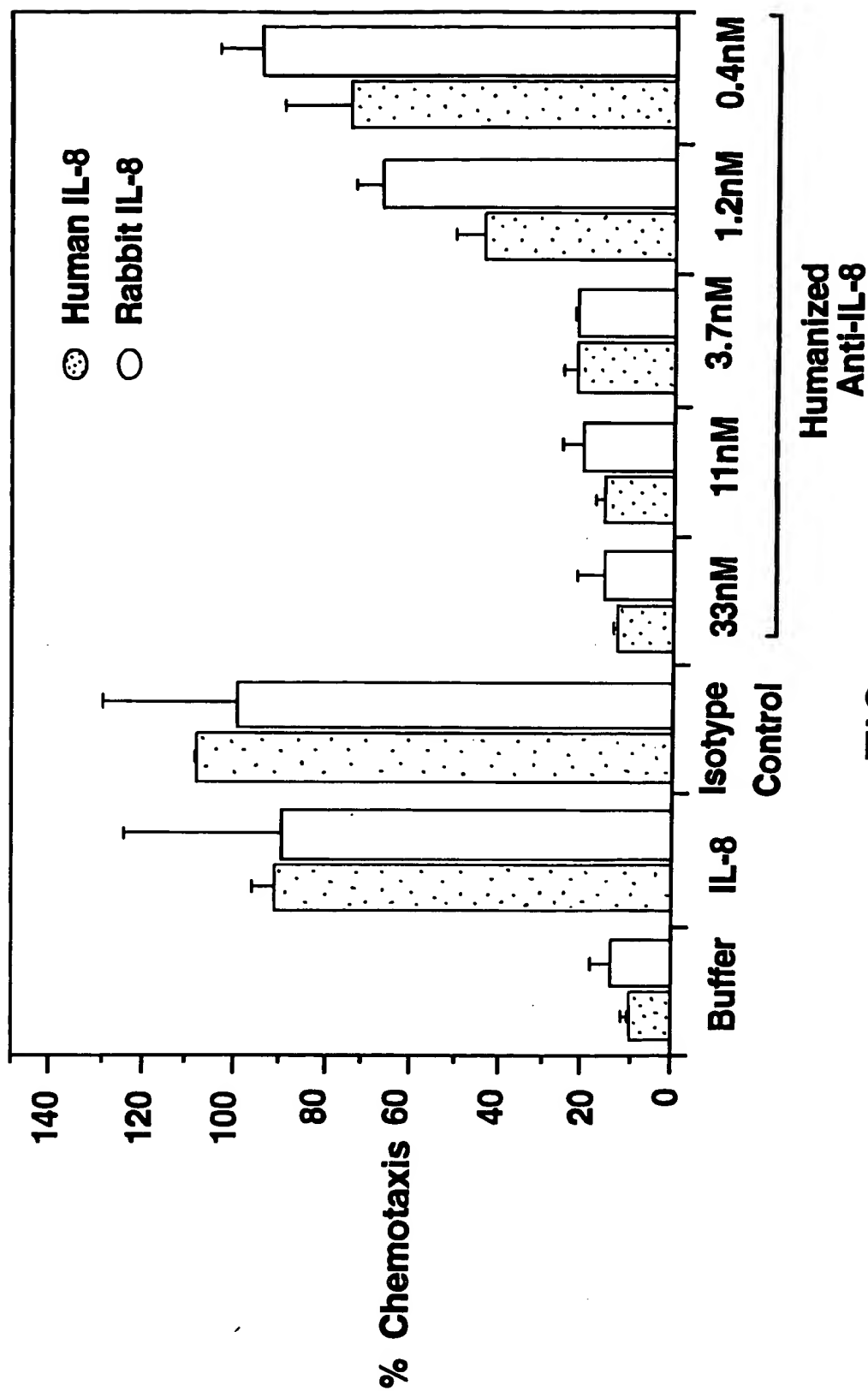


FIG. 46



N35AH1upr

5'-CTAGTGCAGTCTGGCGGTGGCCCTGGTGCAGCCAGGGGGCTCACTCCGTTTGTCTGTGCAGCTTCTGGCTACTCCTTC-3'

N35AH1lwr

5'-TCGAGAAGGAGTAGCCAGAAAGCTGCACAGGACAAACGGAGTGAGCCCCCTGGCTGCACCAGGCCACCGCCAGACTGCAC
AG-3'

Bold indicates nucleotide change destroying PvuII site.

FIG. 47

```

> Wed May 7 18:27:36 1997
> /home/ruby/vc/Immbio/afan/ss.p6G425v11.N35A.choSD
> sites: std
> length: 8120 (circular)
> This has the pSVI backbone with the pRK7 cloning linker (pSVI7) and the intron DHFR(ID)
> made from pSVI.WTSD.D by adding a linearization linker(LL) into the HpaI site

```

```

cac8I
alul
sacI
sacI
hgiJII
hgiAI/aspHI
ec1136II
bsp1286
bsiHKA1
bmyI
banII
taqI
1 TTGAGCTCG CCCGACATTG ATTATTGACT AGAGTCGATC GACAGCTGTG GAATGTGTGT CAGTTAGGCT GTGGAAGATC CCCAGGCTCC CCAGCAGGCA
AAGCTCGAGC GGGCTGTAC TAATTAATCA TCTCAGTAG CTGTGACAC CTTACACACA GTCAATCCCA CACCTTCAG GGTCCGAGG GGTGCTCGT
scrFI mvaI ecorII deaV bstNI apyI[dcmt+] bsaJI bsmFI nlaIV cac8I
seu3AI alul mboI/ndeII[dam-] dpoI[dam+] pvuI/bspCI pleI dpoII[dam-] hinfI taqI[dam-] rmaI mcrI pvuII maeI bsiEI nspBII bfaI taqI[dam-]
sfanI ppulOI nsiI/avaIII nlaIII sphI nspI nspHI cac8I
scrFI mvaI ecorII deaV bstNI apyI[dcmt+] bsaJI bsmFI nlaIV cac8I
101 GAAGTATGCA AAGCATGCAT CTCATTAGT CAGCAACAG GTGTGGAAG TCCCGAGGCT CCCAGCAGG CAGAAGATAG CAAGCATGC ATCTCAATTA
CTTCATACGT TTGCTAGTA GAGTAATCA GTGTTGCTC CACACCTTC AGGGTCCGA GGGTCCGTC CAGGCTGAC GTTCTCATAC GTTCTGATC TAGAGTTAAT
nlaIII styI ncoI bslI deaI acII bsaJI
acII foki acII bsiI acII
201 GTACGCAACC ATAGTCCCGC CCCTAATCC GCCCATCCG CCCTAATC CCCTAATC CGCCGATTC CGCCCATTC CGCCCATTC GTGACTAAT TTTTGTATTT
CAGTGTGTTG TATCAGGCG GGGATTGAG GGGATTGAG GGGATTGAG GGGATTGAG GGGATTGAG GGGATTGAG GGGATTGAG GGGATTGAG GGGATTGAG

```

FIG. 48A





301 TATGCAAGG CCGAGGCCG CTGGCCCTCT GAGCTATTCC AGAAGTAGTG AGGAGCCTTT TTGGAGGCC TAGGCTTTTG CAAAAGCTA GCTTATCCGG
ATACGTCCTCC GGCTCGGCG GAGCCGGAGA CTCGATAAGG TCTTCATCAC TCCTCGGAA AACCTCGG ATCCGAAAC GTTTTCGAT CGATAGGCC

301 TATGCAAGG CCGAGGCCG CTGGCCCTCT GAGCTATTCC AGAAGTAGTG AGGAGCCTTT TTGGAGGCC TAGGCTTTTG CAAAAGCTA GCTTATCCGG
ATACGTCCTCC GGCTCGGCG GAGCCGGAGA CTCGATAAGG TCTTCATCAC TCCTCGGAA AACCTCGG ATCCGAAAC GTTTTCGAT CGATAGGCC

401 CCGGGAACGG TGCATTGGAA CGCGATTCC CGGTGCCAAG AGTGACGTAA GTACGCCCTA TAGAGCGATA AGAGGATTTT ATCCCGCGTG CCATCATGGT
GGCCCTGCCC ACCTAACCTT CGGCTAAGG GGCAGGTTT TCACTGCATT CATGCGGAT ATCTCGTAT TCTCCTAAA TAGGGGCGAC GGATAGTACCA
DHFR ATG*

501 TCGACCATTC AACTGCATCG TCGCCGTCG CCAAAATATG GGGATTGGCA AGAAGGAGA CCTACCTGG CCTCCGCTCA GGAACGAGTT CAAGTACTTC
AGCTGCTAAC TTGACGTAGC AGCGGCACAG GCTTTTATAC CCCTAACCGT TCTTGCCTCT GGATGGGACC GGAGCGGAGT CCTTGTCTCA GTTCATGAAG

FIG. 48B

```

scrFI
mvaI
ecorII
dsav
bstNI
apyl[dcmt+]
sexAI
trulI
hlnfl
dcl mboII tagI
ahallI/draI
msei

601 CAAGAATGA CCACACCTC TTCAGTGGAA GGTAAACAGA ATCTGGTGAT TATGGGTAGG AAAACCTGGT TCTCCATTCC TGAGAAGAT CCACCTTTAA
GTTTCTTACT GGTGTTGGAG AAGTCACCTT CCATTGTCT TAGACCACCTA ATACCCATCC TTTTGGACCA AGAGGTAAAG ACTCTTCTTA GCTGGAATT

eco57I
mboII
earI/esp632I
mnlI
trulI
hlnfl hphI
alwNI[dcmt-]
TATGGGTAGG AAAACCTGGT TCTCCATTCC TGAGAAGAT CCACCTTTAA
GTTTCTTACT GGTGTTGGAG AAGTCACCTT CCATTGTCT TAGACCACCTA ATACCCATCC TTTTGGACCA AGAGGTAAAG ACTCTTCTTA GCTGGAATT

astI
sacI
hglI
hglAI/aspHI
ecII36II
bspI286
bsiHKAII
bmyI
mnlI aluI
mSSI banII
trulI
msei
aseI/asnI/vspI
dcl
trulI
msei
afII/bfII
fokI sfaNI msei
bstXI
TTCTTGCCAA AAGTTTGGAT GATGCCATTAA GACTTATTGA
TCTGTGCTTA ATTATATCAA GAGTCATCTC TTGAGTTTCT TGGTGGTGCT CCTCGAGTAA AAGAAGGTT TTCNAACCTA CTACGGAATT CTGAATAACT

701 AGGACAGAAAT TAATATAGTT CTCAGTAGAG AACTCAAAGA ACCACACCGA GGAGCTCATTT TTCTTGCCAA AAGTTTGGAT GATGCCATTAA GACTTATTGA
TCTGTGCTTA ATTATATCAA GAGTCATCTC TTGAGTTTCT TGGTGGTGCT CCTCGAGTAA AAGAAGGTT TTCNAACCTA CTACGGAATT CTGAATAACT

haeIII/palI
haeI
scrFI
mvaI
ecorII
dsav
bstNI
apyl[dcmt+]
sexAI
trulI
hlnfl
dcl mboII tagI
ahallI/draI
msei

801 ACRACCGGAA TTGGCAAGTA AAGTAGACAT GGTGTTGATA GTTCTGTTTA CCAGGAGGCC ATGATCAAC CAGGCCACCT TAGACTCTTT
TGTTGGCCTT AACCTTTCAT TTCACTCTGA CCAAACTAT CAGCTCCGT CAAGACAAAT GGTCTTCGG TACTTAGTTG GTCCGTGGA ATCTGAGAAA
mspI
hpaII
bsaAI
accI nlaIII
mnlI
bstNI
apyl[dcmt+]
hlnfl
dcl mboII tagI
ahallI/draI
msei

```

FIG. 48C



hgaI
hinli/acyI
ahaiI/baHI
scrFI
mvaI mnlI
ecorII
dsav
bstNI econI
apyI[dcmt+] mnlI
bsaJI belI ddeI
mnlI
901 GTGACGAGGA TCATGCAGGA ATTTCGAAGT GACACGTTTT TCCCGAAGT TGATTTGGGG AAATATAAAC CTCTCCGAGA ATACCAGGC GTCTCTCTG
CACTGTCTCT AGTACGTCTT TAACTTTCA CTGTGCAAAA AGGCTCTTTA ACTAAACCCC TTTATATTTG GAGAGGCTCT TATGGGTCCG CAGGAGAGAC

scrFI
mvaI
ecorII
dsav
bstNI
apyI[dcmt+]
sau96I
avaII
sauI mnlI sfaNI
1001 AGGTCCAGGA GGAAGAGGC ATCAAGTATA AGTTTGAAGT CTACGAGAG AGAAGACTAAC AGGAGATGC TTTCAAGTTC TCTGCTCCOC TCCTAAAGCT
TCCAGGTCTCT CTTTTTCCG TAGTTTCATAT TCAAACTTCA GATGCTCTTC TTTCTGATG TCCTCTACG AAAGTTCAG AGACGAGGGG AGGATTTTCA
*END DHFR

styI
bsaJI
sau3AI
mboI/ndeII[dam-]
dpmI[dam+]
dpmII[dam-]
alwI[dam-]
bstYI/xhoII
cac8I
ppu10I
nslI/avaII
1101 ATGCATTTT ATAGACCAT GGGACTTTTG CTGGCTTTAG ATCCCTTGG CTTCGTTAGA AGCAGCTAC AATTATACA TAACCTTATG TATCATACAC
TACGTAAAAA TATTCTGSTA CCTGTGAAC GACCGAATC TAGGGGAAC GAGCAATCT TCGCTCGATG TTAATTATCT ATTGGAATAC ATAGTATGTC
sau96I
avaII
asuI
scrFI
mvaI
ecorII

FIG. 48D

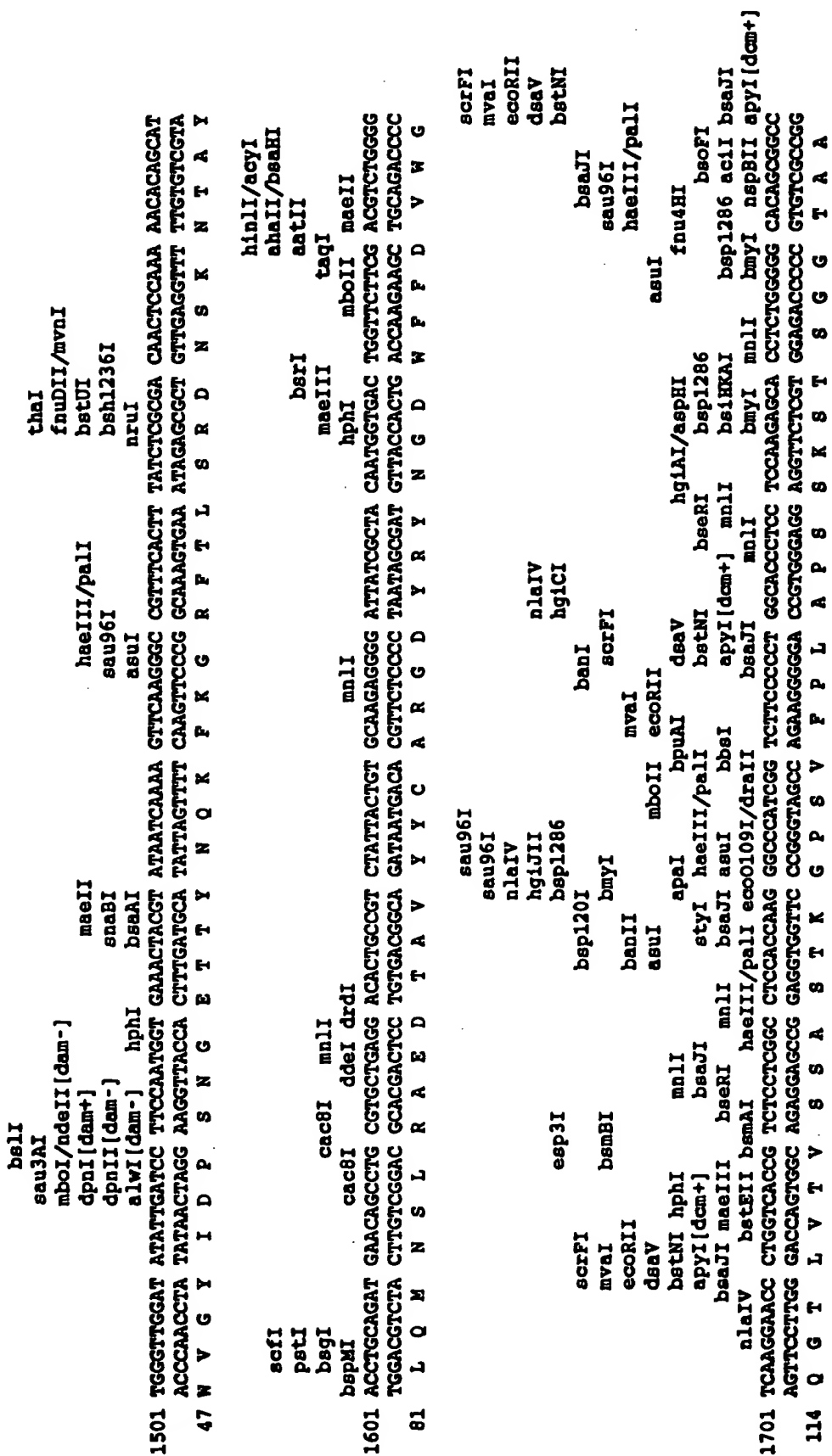


1201 ATACGATTAA GGTGACACTA TAGATAACAT CCACTTTGCC TTCTCTCCA CAGGTGTCCA CTCCAGGTC CAACTGCACC TCGTTCTAT CGATTGAAT
TATGCTAAT CCACTGTAT ATCTATTGTA GGTGAACCG AAGAGAGGT GTCCACAGT GTCCACAGT GGTGACGTTGAGG AGCCAGATA GCTACTTAA
seq from pR6G425VH: Cla-AVII⁻

1301 CCACCATGGG ATGTCATGT ATCATCTTT TTCTAGTAGC AACTGCACT CGAGTACAT CAGAGTTCA GCTAGTGCAG TCTGGCGTG CGCTGTGCA
GGTGTACCC TACCAGTACA TAGTAGGAAA AAGATCATCG TTGACGTTGA CCTCATGTAA GTCTCAAGT CGATCACGTC AGACCCGAC CGACCACTT
E V Q L V Q S G G G L V Q

1401 GCCAGGGGC TCACTCGCTT TGTCTGTGC AGTTCTGCG TACTCTTCT CGAGTCACTA TATGCTAGT GTCCGTGAG CCCCCTGTA GGGCTGGAA
CGTCCCGG AGTGAGGCAA ACAGGACAG TCGAGGACG ATGAGGACG GCTCAGTAT ATACGTACC CAGGAGTCC GGGGCCCAT CCCGACCTT
14 P G G S L R L S C A A S G Y S F S S H Y M H W V R Q A P G K G L E

FIG. 48E





```
scrFI      hinpI      hgiAI/aspHI      hgiAI/aspHI      hgiAI/aspHI
mvaI      nlaIV      nari      bsp1286      bsp1286
ecoriI      kasi      hinII/acyI      bmyI      nspi
dsav      hgiCI      cac8I      hpaII      hpaII
bstNI      haeII      baeII      baeII      baeII
bsaFI      baeII      baeII      baeII      baeII
apyl[dcn+]      baeII      baeII      baeII      baeII
fnu4HI      baeII      baeII      baeII      baeII
bsaFI      baeII      baeII      baeII      baeII
bbVI      baeII      baeII      baeII      baeII
1801 CTGGGCTGCC TGGTCAAGGA CTACTTCCC GAAACCGTGA CGGTGTGTG GAACTGAGG GAACTGAGG GAACTGAGG GAACTGAGG GAACTGAGG
GACCCGAGCG ACCAGTTCCT GATGAAGGG CTTGGCCACT GCCACAGCAC CTTGACTCCG CGGGACTGCT CGGGACTGCT CGGGACTGCT CGGGACTGCT
147 L G C L V K D Y F P E P V T V S W N S G A L T S G V H T F P A V L Q

fnu4HI      fnu4HI      fnu4HI      fnu4HI      fnu4HI
bsaFI      bsaFI      bsaFI      bsaFI      bsaFI
dcl pleI      dcl pleI      dcl pleI      dcl pleI      dcl pleI
nli hinfI      nli hinfI      nli hinfI      nli hinfI      nli hinfI
eco8II      eco8II      eco8II      eco8II      eco8II
bsu36I/mstII/sauI dcl pleI      bmyI      bmyI      bmyI
1901 AGTCTCTCAG ACTTACTCC CTCAGCAGCG TGGTACTGT GCTCTAGC AGCTTGGGCA CCCAGACCTA CATCTGCAAC CATCTGCAAC CATCTGCAAC CATCTGCAAC
TCAGGAGTCC TGAGATGAGG GAGTGTGCG ACCACTGACA CGGAGATCG TCGAACCCGT GGTCTGCTGAT GTAGAGGTG CACTTACTGT TCGGCTGCTT
181 S S G L Y S L S S V V T V P S S S L G T Q T Y I C N V N H K P S N

fnu4HI      fnu4HI      fnu4HI      fnu4HI      fnu4HI
bsaFI      bsaFI      bsaFI      bsaFI      bsaFI
dcl pleI      dcl pleI      dcl pleI      dcl pleI      dcl pleI
nli hinfI      nli hinfI      nli hinfI      nli hinfI      nli hinfI
eco8II      eco8II      eco8II      eco8II      eco8II
bsu36I/mstII/sauI dcl pleI      bmyI      bmyI      bmyI
2001 CACCAAGTGG GACAGAGAAG TTGAGCCCA ATCTGTGAC AAAACTACA CATGCCACC GTGCCAGCA CTTGACTCC TGGGGGACC GTGAGTCTTC
CTGTTTCCAC CTGTTTCTTC AACTCGGTTT TAGAACACTG TTTTGTGTGT GTAGAGGTG CACGGGTGTT CACGGGTGTT CACGGGTGTT CACGGGTGTT CACGGGTGTT
214 T K V D K K V E P K S C D K T H T C P P C P A P E L L G G P S V F

fnu4HI      fnu4HI      fnu4HI      fnu4HI      fnu4HI
bsaFI      bsaFI      bsaFI      bsaFI      bsaFI
dcl pleI      dcl pleI      dcl pleI      dcl pleI      dcl pleI
nli hinfI      nli hinfI      nli hinfI      nli hinfI      nli hinfI
eco8II      eco8II      eco8II      eco8II      eco8II
bsu36I/mstII/sauI dcl pleI      bmyI      bmyI      bmyI
2001 CACCAAGTGG GACAGAGAAG TTGAGCCCA ATCTGTGAC AAAACTACA CATGCCACC GTGCCAGCA CTTGACTCC TGGGGGACC GTGAGTCTTC
CTGTTTCCAC CTGTTTCTTC AACTCGGTTT TAGAACACTG TTTTGTGTGT GTAGAGGTG CACGGGTGTT CACGGGTGTT CACGGGTGTT CACGGGTGTT CACGGGTGTT
214 T K V D K K V E P K S C D K T H T C P P C P A P E L L G G P S V F
```

FIG. 48G



[illegible]

FIG. 48I



scrFI
ncII
mspI
hpalI
dsav
bsmAI
belI cauII
2701 TCCTGTCTC CGGTAATG AGTGGACGG CCTAGAGTC GACTGCAGA AGCTGGCGG CCATGGCCCA ACTTGTTAT TGCAGCTTAT AATGGTTACA
AGGACAGAG GCCCATTTAC TCACCGTGC GGGATCTCAG CTGGACGTCT TCGACCGGC GSTACCGGT TGAACAATA AGTCGRATA TTACCAATGT
447 S L S P G K O

sa96I
acII haeIII/palI
fnu4HI asuI
bsoFI nlaIII
sfII styI
eaeI ncoI
cfri dsal
aluI haeIII/palI
aluI bglI bsaJI
2801 AATAAGCAA TAGCATCACA AATTTCACAA ATAAAGCAAT TTTTCACGT CATTACAGTT GTGGTTGTC CAATCATC ATGTATCTT ATCATGCTG
TTATTTCGTT ATCGTAGTGT TTAAGTGT TATTTCGTAA AAAAGTGAC GTAGATCAA CACCAACAG GTTGTAGTAG TTACATAGNA TAGTACAGAC

sa3AI
mboI/ndeII(dam-)
dpnI(dam+)
dpnII(dam-)
pvuI/bspCI
mori
bsiEI
taqI(dam-) tru9I
claI/bsp106(dam-)
bspDI(dam-) mseI
sau3AI xmnI
mboI/ndeII(dam-)
dpnI(dam+) asp700
dpnII(dam-) aseI/aseI/vspI bsaJI
2901 GATCGATCGG GAATTAATTC GCGGACGAC CATGGCCTGA AATAACCTCT GAAGAGGAA CTGTGTTAGG TACCTTCTGA GCGGAAAGA ACCATCTGT
CTAGCTAGCC CTTAATTAAG CCGGCTGTG GTACCGGACT TTATTGGAGA CTTCCTCTT GAACCAATCC ATGGAGACT CCGCTTCT TGGTAGACAC

real
osp6I
nlaIV
kpnI
hgiCI
bani
asp718 mnlI
acc65I ddeI acII

zmaI
maeI
bmi bfaI
nlaIII alwI(dam-)

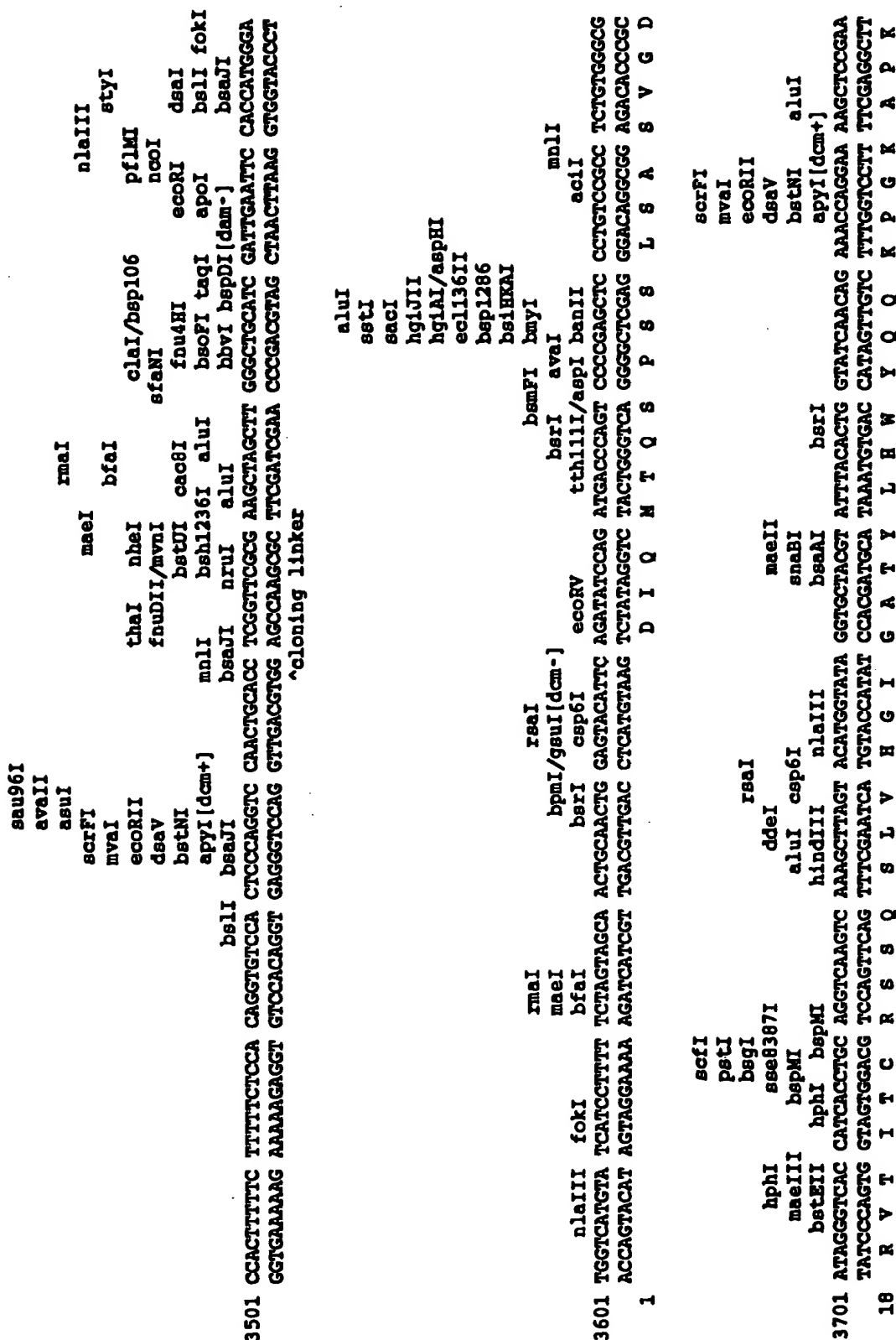
FIG. 48J

[illegible]

FIG. 48K

[illegible]

FIG. 48L





mspI
hpaII
bsaI
bsaWI
sau3AI
mboI/ndeII(dam-)
dpsI(dam+)
dpsII(dam-)
alwI(dam-)
nlaIV
bstYI/xhoII
bamHI
alwI(dam-)
bsmFI
tfII
hinFI
taqI
clalI/bsp106
pleI
bspDI(dam-)
hinFI
bsmFI
bpmI/gsuI(dam-)
3801 ACTACTGATT TACAAGTAT CCAATCGATT CTCTGGAGTC CCTTCTGGCT TCTCTGATC CGGTTCTGG AGGATTTCA CTCTGACCAT CAGCAGTCTG
TGATGACTAA ATGTTTCATA GGTAGCTAA GAGACCTCAG GGAAGAGCGA AGAGACCTAG GCCAAGACCC TGCCTAAGT GAGACTGGTA GTCGTGAGAC
51 L L I Y K V S N R F S G V P S R F S G S G S G T D F T L T I S S L
fnu4HI
bsoFI
bbvI
scfI
pstI
bsgI
rsal
csp6I
nlaIV
kpnI styI
hgiCI
banI bsaJI
asp718
acc65I
sau3AI
mboI/ndeII(dam-) fnu4HI
dpsI(dam+) bsoFI
dpsII(dam-) bbvI
3901 CAGCCAGAAG ACTTCGCAAC TTATTACTGT TCACAGAGTA CTGATGTCCC GCTCAGCTTT GCACAGGGTA CCAAGGTGGA GATCAACGA ACTGTGCGTG
GTGGTCTTC TGAAGCGTTG AATAATGACA AGTGCTCAT GAGTACAGGG CGAGTGCAA OCTGTCCCAT GTTCCACCT CTAGTTTGT TGCACCGGAC
84 Q P E D F A T Y Y C S Q S T H V P L T F G Q G T K V E I K R T V A A
mboII
bpuAI
bbeI
mboII acII
xmnI
asp700
cseBI
acII
bsmFI
bsaI
nlaIII
scaI
rsal
csp6I
4001 CAGCATCTGT CTTCATCTTC CCGCCATCTG ATGAGCAGTT GAATCTGGA ACTGCTCTG TTGTGTGCTT GCTGATTAAC TTCTATCCCA GAGAGGCCAA
GTGGTAGACA GAAGTAGAAG GGGGTAGAC TACTCGTCAA CTTAGACCT TGAAGAGAC AACACACGGA CGACTTATTG AAGTAGGTT CTCTCCGTT
118 P S V F I F P P S D E Q L K S G T A S V V C L L N N F Y P R E A K
haeIII/palI
haeI
mnlI

FIG. 48N

scrFI
 mval
 ecorII
 dsav
 bstNI
 apyI[dcn+]
 mnli
 belI
 maeIII
 bsaJI
 maeIII
 fnu4HI
 ddel bsoFI
 scFI mnli bbvI
 4101 AGTACAGTGG AAGGTGGATA ACGCCTCCA ATCGGTAAC TCCAGGAGA GTGTACACAGA GCAGGACRGC AAGACACAGA CCTACAGCCT CAGCAGCACC
 TCATGTCACC TTCACCTAT TCGCGGAGGT TAGCCCATTG AGGCTCTCT CACAGTGTCT CAGTCTCTCG TTCCTGTCTG GATGTCGGA GTCTGTCTGG
 151 V Q W K V D N A L Q S G N S Q E S V T E Q D S K D S T Y S L S S T
 sstI
 sacI
 hgiJII
 hgiAI/aspHI
 ecl136II
 bsp1286
 bsiHKAI
 bmyI
 ddel cac8I
 haeIII/pali
 sau96I aluI
 asuI banII
 hphi
 ecoO109I/draiI
 maeIII aluI
 4201 CTGACGTGA GCAAGCAGA CTCAGAGAA CACAAGTCT ACGCTGCGA AGTCACCAT CAGGCGCTGA GTCTGCGCTG CACAAGACG TTCACACAGG
 GACTGCCACT CGTTTCGTCT GATGCTCTTT GTGTTTCAGA TCGCGACGCT TCAGTGGGTA GTCCCGGACT CGAGCGGGCA GTGTTTCTCG AAGTTGTCC
 184 L T L S K A D Y E K B K V Y A C E V T H Q G L S S P V T K S F N R G
 ddel
 celII/espI
 blpI/bpul102I
 hgaI
 accI cac8I
 maeIII
 sau96I
 haeIII/pali
 fnu4HI
 asuI
 bsoFI nlaIII
 sfil styI
 aluI haeIII/pali
 hindIII bgli ncoI
 tru9I eaeI dsai
 msel cfrI bsaJI
 sau96I
 acil haeIII/pali
 fnu4HI
 asuI
 bsoFI nlaIII
 sfil styI
 aluI haeIII/pali
 hindIII bgli ncoI
 tru9I eaeI dsai
 msel cfrI bsaJI
 4301 GAGAGTCTTA AGCTTGGCCG CCATGCGCCA ACTTGTTTAT TCGAGCTTAT AATGCTTACA AATAAGCAGA TAGCATCACA AATTTCACAA ATTAAGCAT
 CTCTCACAAT TCGAACCGC GGTACCGGT TGAACAAATA ACSTOGAATA TTACCAATGT TTATTCTT ATCTAGTGT TTAAGTGT TATTCTGTA
 218 E C O
 sfanI apoI

FIG. 480



```

sau3AI
mboI/ndeII[dam-]
dpmI[dam+]
dpmI[dam-]
pvuI/bspCI
mcrI
bsiEI
taqI[dam-]
claiI/bsp106[dam-]
bspDI[dam-] tru9I
sau3AI mseI
mboI/ndeII[dam-]
dpmI[dam+] xmiI
dpmI[dam-]
dpmI[dam-] asei/asnI/vspI bsaJI
nlaIII alwI[dam-] asp700 hhaI/cfoI nlaIII
4401 TTTTTCACATG CATTCTAGTT GTGGTTTGTG CAAACTCATC AATGTATCTT ATCAGTCTG GATCGATCGG GAATTAATTC GCGCAGCAC CATGGCCTGA
AAAAAGTCAC GTACATCA GTTTGAGTAG TTACATAGAA TAGTACAGAC CTAGCTAGCC CTTAATTAAG CCGCGTCTG GTACCGACT
~sv40 origin

rmalI mnlI
maeI
bsmI bfaI
4401 TTTTTCACATG CATTCTAGTT GTGGTTTGTG CAAACTCATC AATGTATCTT ATCAGTCTG GATCGATCGG GAATTAATTC GCGCAGCAC CATGGCCTGA
AAAAAGTCAC GTACATCA GTTTGAGTAG TTACATAGAA TAGTACAGAC CTAGCTAGCC CTTAATTAAG CCGCGTCTG GTACCGACT

rsalI
csp6I
nlaIV
kpnI
hgiCI
banI
asp718 mnlI
acc65I ddeI aciI
4501 AATAACTCT GAAGAGGAA CTTGGTTAGG TACCTTCTGA GCGGGAAGA ACCAGCTGTG GAATGTGTGT CAGTTAGGT GTGGAAGTC CCCAGGCTCC
TTATTGAGA CTTTCTCCTT GAACCAATCC ATGGAAGACT CCGCCTTCT TGTGACAC CTTACACACA GTCAATCCCA CACCTTTCAG GGTCCGAGG

alulI
pvuII
nspBII
4501 AATAACTCT GAAGAGGAA CTTGGTTAGG TACCTTCTGA GCGGGAAGA ACCAGCTGTG GAATGTGTGT CAGTTAGGT GTGGAAGTC CCCAGGCTCC
TTATTGAGA CTTTCTCCTT GAACCAATCC ATGGAAGACT CCGCCTTCT TGTGACAC CTTACACACA GTCAATCCCA CACCTTTCAG GGTCCGAGG

sfanI
ppu10I
nslI/avaIII
nlaIII
sphi
nspi
nspHI
cac8I
4601 CCAGCAGGCA GAAGTATGCA AAGCATGCAT CTCAATTAGT CAGCAACCAG GTGTGGAAG TCCCGAGGT CCCAGCAGG CAGAAGTATG CAAAGCATGC
GGTCGTCCGT CTTACATCGT TTGTAGCTA GAGTTAATCA GTCTTGGTC CACACCTTC CACACCTTC AGGGTCCGA GGGGTCTGTC GTCTTCATAC GTTCTGATG

scrFI
mvalI
ecorII
dcaV
bstNI
apyI[dcm+]
bsaJI
4601 CCAGCAGGCA GAAGTATGCA AAGCATGCAT CTCAATTAGT CAGCAACCAG GTGTGGAAG TCCCGAGGT CCCAGCAGG CAGAAGTATG CAAAGCATGC
GGTCGTCCGT CTTACATCGT TTGTAGCTA GAGTTAATCA GTCTTGGTC CACACCTTC CACACCTTC AGGGTCCGA GGGGTCTGTC GTCTTCATAC GTTCTGATG

sfanI
ppu10I
nslI/avaIII
nlaIII
sphi
nspi
nspHI
cac8I
4601 CCAGCAGGCA GAAGTATGCA AAGCATGCAT CTCAATTAGT CAGCAACCAG GTGTGGAAG TCCCGAGGT CCCAGCAGG CAGAAGTATG CAAAGCATGC
GGTCGTCCGT CTTACATCGT TTGTAGCTA GAGTTAATCA GTCTTGGTC CACACCTTC CACACCTTC AGGGTCCGA GGGGTCTGTC GTCTTCATAC GTTCTGATG
```

FIG. 48P

4701 ATCTCAATTA GTCAGCAACC ATATGCCCGC CCCTAACTCC GCCATCCCG CCGCATCTCT CGCCCATCTT CCGCCCATG GCTGACTAAT
TAGAGTTAAT CAGTCGTTGG TATCAGGGCG GGGATTGAG GCGGATTGAG CCGGTCAAG GCGGGTAAGA GCGGGGTAC CGACTGATTA

4801 TTTTATTAT TATGCAGAG CCGAGCCGC CTCGGCTCT GAGCTATTC AGAGTAGTG AGGAGCTTT TTTGGAGCC TAGGCTTTG CAARAAGCTG
AAAAAATAA ATACGTCCTC GGCTCCGCG GAGCCGAGA CTCGATAAGG TCTTCATCAC TCCTCGAAA AACCTCGG ATCCGAAAC GTTTTCGAC
start pUC118

4901 TTACCTCAG CGSCCGTTA ATTAGCCGC GCCATTAA TCTGCAGT AACAGCTTG CACTGCCGT CGTTTACAA CGTCGTGACT GGGAAAOCC
AATGGAGTC GCGCGCAAT TAATCCGCG CGGTAAAT AGCAGTCCA TTCTCGAACC GTGACGGCA GCAAAATGTT GCAGCACTGA CCTTTTGGG

FIG. 48Q

[illegible]

FIG. 48R

[illegible]

FIG. 48S

[illegible]

FIG. 48T

FIG. 48U



6601 CGACGAGCGT GACACCAAGA TGCCAGCAGC AATGCAACCA AACTATTAAAC TGGCGAATA CTACTCTAG CTCCCGGCA ACRATTAATA
GCTGCTCGCA CTGTGGTGCT ACGGTGCTG TACCGCTGT TGCACGCGT TTGATAATTG ACCGCTTGAT GAATGAGATC GAAGGCGCGT TGTAAATTAT
6701 GACTGGATGG AGGCGGATRA AGTTGCAGGA CCACCTTCTGC GCTCGGCCCT TCCGCTGGC TGGTTTATG CTGATAAATC TGGAGCGCGT GAGCGTGGGT
CTGACCTACC TCCGCTATT TCAACGTCTT GGTGAAGACG CGAGCCGGGA AGGCCGACCG ACCAATAAC GACTATTAG ACTCGGCCA CTCGCAACCA
6801 CTCGCGGTAT CATTGACGCA CTGGGGCCAG ATGGTAAGCC CTCGCTATC GTAGTATCT ACACGACGG GAGTCAGGCA ACTATGGATG AACGAATAG
GAGCGCCATA GTAACGTCTT GACCCCGTC TACCATTGG GAGGCGATG CATCATAGA TGTGCTGCC CTCAGTCCGT TGATACCTAC TTGCITTATC
6901 ACAGATCGCT GAGATAGTG CCTCACTGAT TAAGCAATGG TAACGTGTCAG ACCAAGTTA CTCATATA CTTAGATTG ATTTAAACT TCATTTTAA
TGTCTAGCGA CTCTATCCAC GGAGTGACTA ATTGTAACC ATTGACAGTC TGGTTCAAT GAGTATAT GAAATCTAC TAAATTTGA AGTAAAAAT
7001 TTTAAAGGA TCTAGGTGAA GATCCTTTT GATAATCTCA TGACCAAAAT CCCTTAACGT GAGTTTCTG TCCACTGAGC GTCAGACCCC GTCAGAAAGA
AAATTTCTCT AGATCCACTT CTAGGAAAA CTATTAGAT ACTGGTTTGA GGGAAATGCA CTCAAAAGCA AGGTGACTCG CAGTCTGGG CATCTTTCT

FIG. 48V

sau3AI
mboII[dam-]
sau3AI mboI/ndelII[dam-] thai
mboI/ndelII[dam-] fndII/mvni
dplI[dam+] dplI[dam+] bstUI cacBI
dplII[dam-] dplII[dam-] bsh1236I fnu4HI
bstYI/xhoII alwI[dam-] hinPI bsoFI
alwI[dam-] bstYI/xhoII hhai/fofI bbvI
7101 TCAAGGATC TTCTTGAGAT CCTTTTTC TCGCGGTAAT CTGCTGCTTG CAACAARAAA AACACCGCT ACCAGCGGT GTTGTGTTGC CGGATCAAGA
AGTTTCCTAG AAGAACTCTA GMAAAAAAG ACGCGCATTA GAGACGGAAC GTTTGTGTTT TTGTCGCCA TGGTCGCCAC CAAACAACG GCCTAGTTCT

7201 GCTACCAACT CTTTTCCGA AGGTAACCTGG CTTACGAGA GCCAGATAC CAATACTGT CCTTCTAGTG TAGCCGTAGT TAGGCCACCA CTTCAAGAAC
CGATGGTGA GAAAAGGCT TCCATTGACC GAAGTCGTCT CGCGTCTATG GTTTATGACA GGAAGATCAC ATCGGCATCA ATCCGGTGGT GAAGTTCTTG

7301 TCTGTAGCAC CGCTACATA CCTCGTCTG CTAATCTGT TACCAGTGC TGTGCCAGT GCGGATAAGT CGTGTCTTAC CGGTTGGAC TCAAGACGAT
AGACATCGTG CGCGATGTAT GGAGCGAGAC GATTAGGACA ATGTCCACCG ACGAGGTCA CCGCTATTCA GCACAGAATG GCCCAACCTG AGTTCGTCTA

7401 AGTTACCGA TAAGGCGCAG CGGTGGGCT GAACGGGGG TTCTGTGACA CAGCCAGCT TGGAGCGAAC GACCTACACC GAACTGAGAT ACCTACAGCG
TCATGGGCT ATTCCCGTC GCCAGCCGA CTTGCCGCCC AAGCACGTGT GTGGGTGCA ACCTGCTTG ACCTGCTG TGGATGCGC

FIG. 48W



7501 TGAGCAATTCA GAAAGCGCCA CGCTTCCCGA AGGAGAGAAAG GCGGACAGGT ATCCGGTAAG CGGCAGGGTC GGAACAGGAG AGCGCACGAG GGAGCTTCCA
ACTCGTAACT CTTTCGCGGT GCGAAGGGCT TCCCTCTTTC CGCTGTCCA TAGGCCATTC GCCGTCCAG CCTGTCTC TCCTGCTC CTCGAAGGT

scriFI mvaI ecorII dsav bstNI
hinPI hhaI/cfoI haeII
mspI hpaII fnu4HI bsaI
belI bsoFI hlnPI mnlI hhaI/cfoI aluI apyI(dcm+)

7601 GGGGGAAGC CTGCTATCT TTATAGTCT GTCCGGTTTC GCCACCTCTG ACTGAGCGT CGATTTTGT GATCTCTGTC AGGGGGCGG AGCCTATGGA
CCCCCTTTC GGACCATAGA AATATCAGGA CAGCCCAAG CGGTGGAGAC TGAATCGCA CACTAAGACA CTACGAGCAG TCCCCCGCC TCAGTACCT

scriFI mvaI ecorII dsav bstNI
hapI hpaII fnu4HI bsaI
belI bsoFI hlnPI mnlI hhaI/cfoI aluI apyI(dcm+)

7701 AAAAGCGCAG CAACGCGGC TTTTACGGT TCCTGGCCTT TTGCTGCACA TGTCTTTC TCCTATATCC CCTGATCTG TGGATAACCG
TTTTGCGTC GTTGGCGCG AAAATGCGA AGGACCGGA AACGACCGA AACGAGTGT ACAGGAAGG ACCAATAGG GGAATAAGAC ACCTATTGGC

scriFI mvaI ecorII dsav bstNI
hapI hpaII fnu4HI bsaI
belI bsoFI hlnPI mnlI hhaI/cfoI aluI apyI(dcm+)

7801 TATTACGCG TTTGAGTGAG CTGATACCG TCAGCGCAGC GGAACGACCG AGCGCAGCA GTCACTGAGC GAGGAGCGG AAGAGCGCC AATACGCAAA
ATAATGCGG AACTCACTC GACTATGCG AGCGGCGTC GCTTCTGTC TCCTGCTGCT CAGTCACTG CTCTTCTGCC TTCTCGCGG TTATGCGTTT

scriFI mvaI ecorII dsav bstNI
hapI hpaII fnu4HI bsaI
belI bsoFI hlnPI mnlI hhaI/cfoI aluI apyI(dcm+)

FIG. 48X



```

      thal
      fnuDII/mvni
      betOI
      beh1236I
      hinPI
      hhal/cfoI
      thal
      fnuDII/mvni          cac8I
      betOI haeIII/palI    aluI
      beh1236I             tru9I pvuII
      balI eaeI tfII aseI/asnI/vspI
      aciI cfrI hinFI mseI nspBII
7901 CCGCGCTCTCC CCGCGCTTG CCGGATTTCAT TAATCCAGCT GGCACGACAG GTTCCCGAC TGGAAAGCGG GCAGTGAGCG CAACGCAATT AATGTGAGTT
      GCGCGAGAGG GCGCGCAAC CCGCTAGTA ATTAGGTGA CCGTGCTGTC CAAAGGGCTG ACCTTTGCGC CGTCACTCGC GTTGCCTAA TTACACTCAA
      mnlI
      aciI
      cac8I
      acII
      berI
      cac8I
      acII
      hinPI
      hhal/cfoI
      aseI/asnI/vspI
      mseI
      tru9I
      maeIII

      scrFI
      mvaI
      ecorII
      dsav
      nlaIV betNI
      hgiCI apyI[dm+]
      banI beaJI
      mnlI
8001 ACCTCACTCA TTAGGCACCC CAGGCTTTAC ACTTTATGCT TCCGGCTCGT ATGTTGTGTG GAATTGTGAG CCGATAACAA TTTCACACAG GAAACAGCTA
      TGGAGTGAGT AATCCGTGGG GTCCGAATG TGAAATACGA AGGCCGAGCA TACAACACAC CTTACACTC GCCTATTGTT AAAGTGTGTC CTTGTGCGAT
      mspI
      hpaII
      acII
      bsrBI
      aluI
```

FIG. 48Y



```
tru9I
mseI
aseI/asnI/vspi
xmnl
nlaiII asp700
8101 TGACCATGAT TACGAATTAA
ACTGGTACTA ATGCTTAATT

>length: 8120

aatII(GACGTC): 1690 5947
acc65I(GGTACC): 2969 3967 4529
accI(GTMRAC): 823 1039 2738 4237
aciI(CCGC): 217 229 238 250 260 271 317 422 454 485 574 1385 1795 1871 2248 2250 2758 2982
3167 3179 3188 3200 3210 3221 3267 3372 3404 3449 3686 3949 4021 4318 4542 4727
4739 4748 4760 4770 4781 4827 4910 4914 5070 5127 5153 5166 5203 5217 5220 5248
5275 5680 5699 5741 5751 5790 5979 6026 6125 6234 6311 6355 6476 6522 6713 6804
7166 7175 7310 7420 7541 7560 7687 7715 7806 7827 7834 7877 7901 7911 7967 8070
see hinII
acyI
afII/dfrI(CTTAAG): 786
afIIII(ACRYGT): 932 7758
ageI(ACCGGT): 1833
ahaiI/bsaHI(GRCGYC): 988 1690 1858 5117 5947 6329
ahaiI/draI(TTTAA): 696 4935 6290 6982 7001
ahdI/eamI105I(GACNNNNNGTC): 2087 6865
alul(AGCT): 5 44 332 386 390 753 1097 1165 1370 1431 1951 2603 2751 2784 3282 3336 3340
3562 3566 3676 3733 3792 4270 4288 4311 4344 4554 4842 4896 4954 5047 5333 5590
5803 5822 6516 6579 6679 7200 7457 7593 7819 7937 8096
alw44I/snoI(GTGCAC): 1876 5651 6198 7444
```

FIG. 48Z

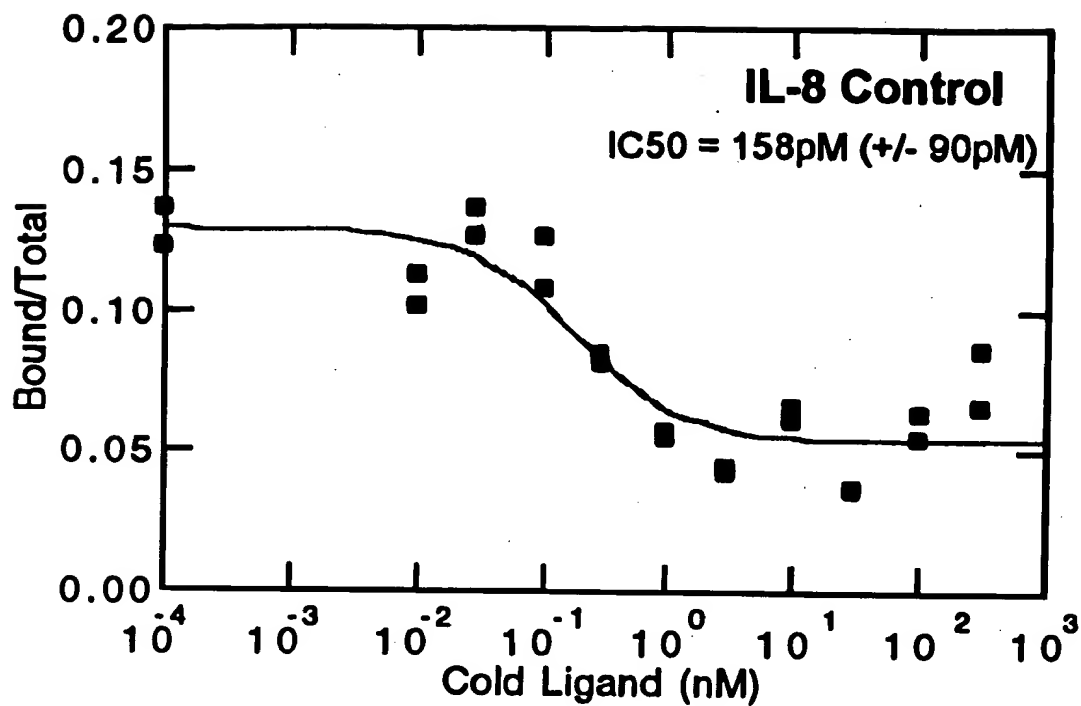


FIG. 49A

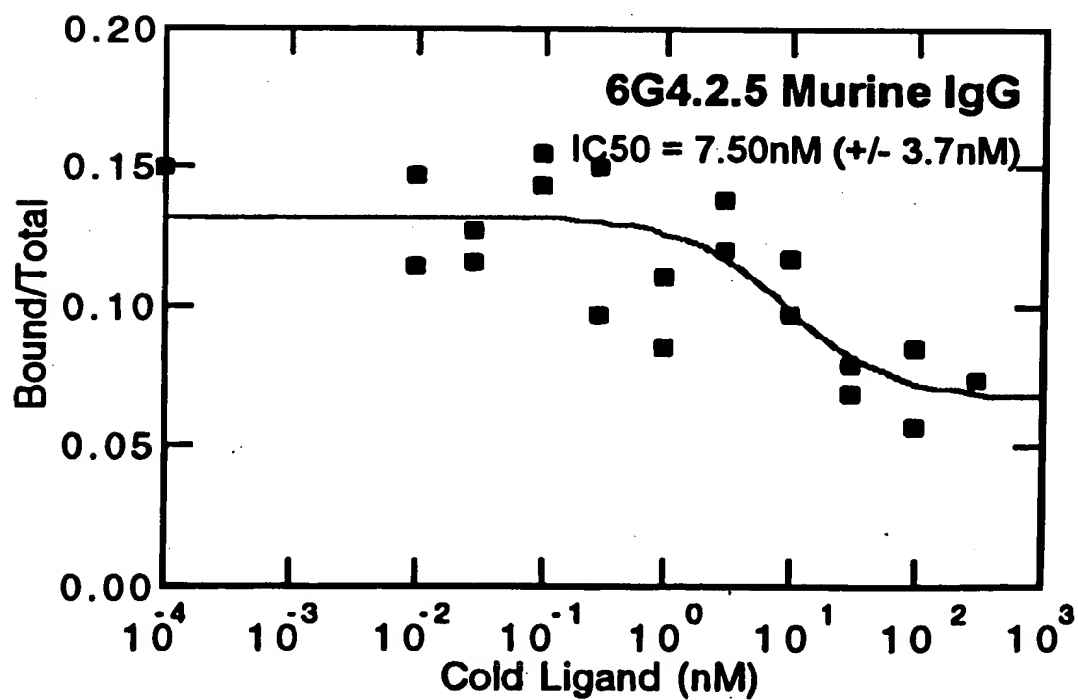


FIG. 49B

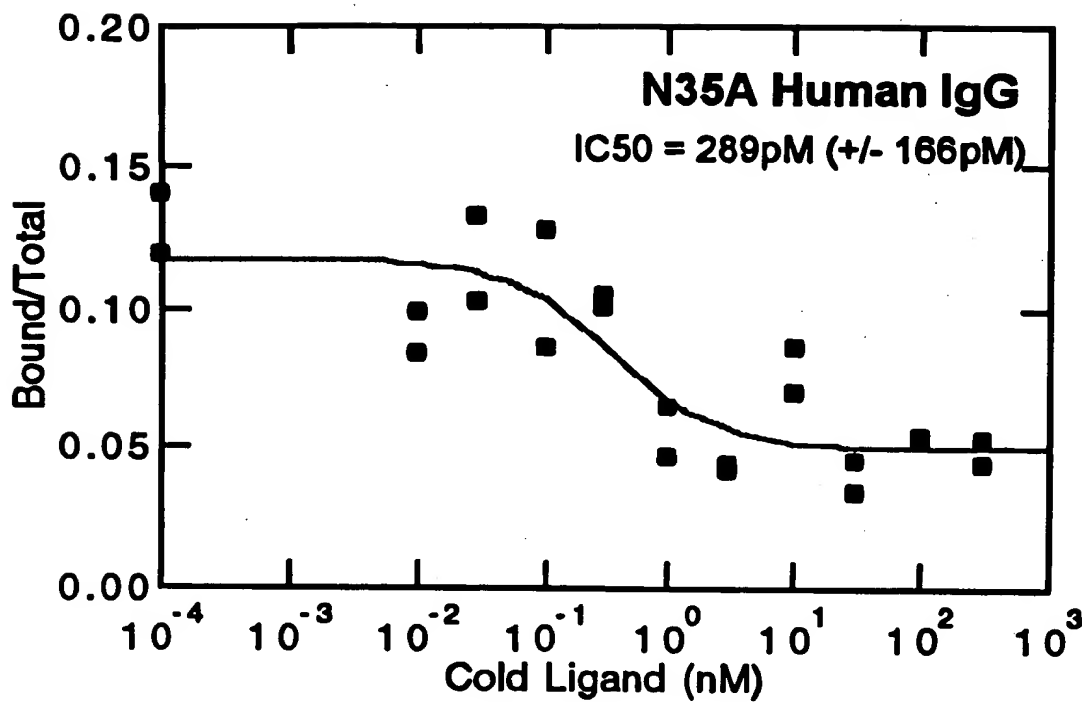


FIG. 49C

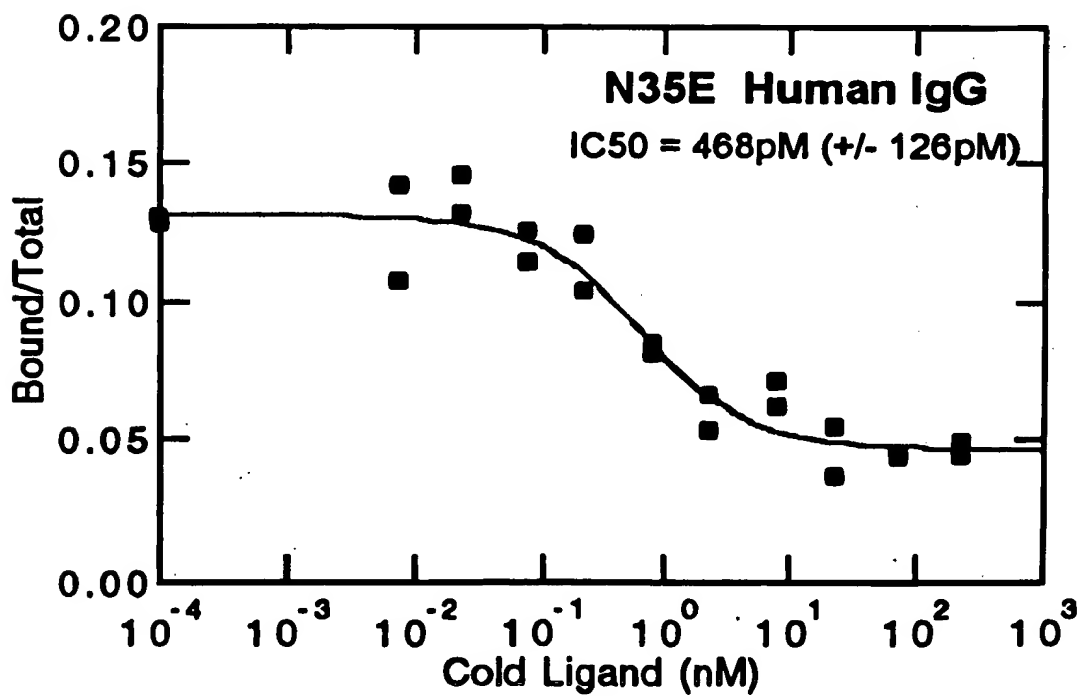


FIG. 49D

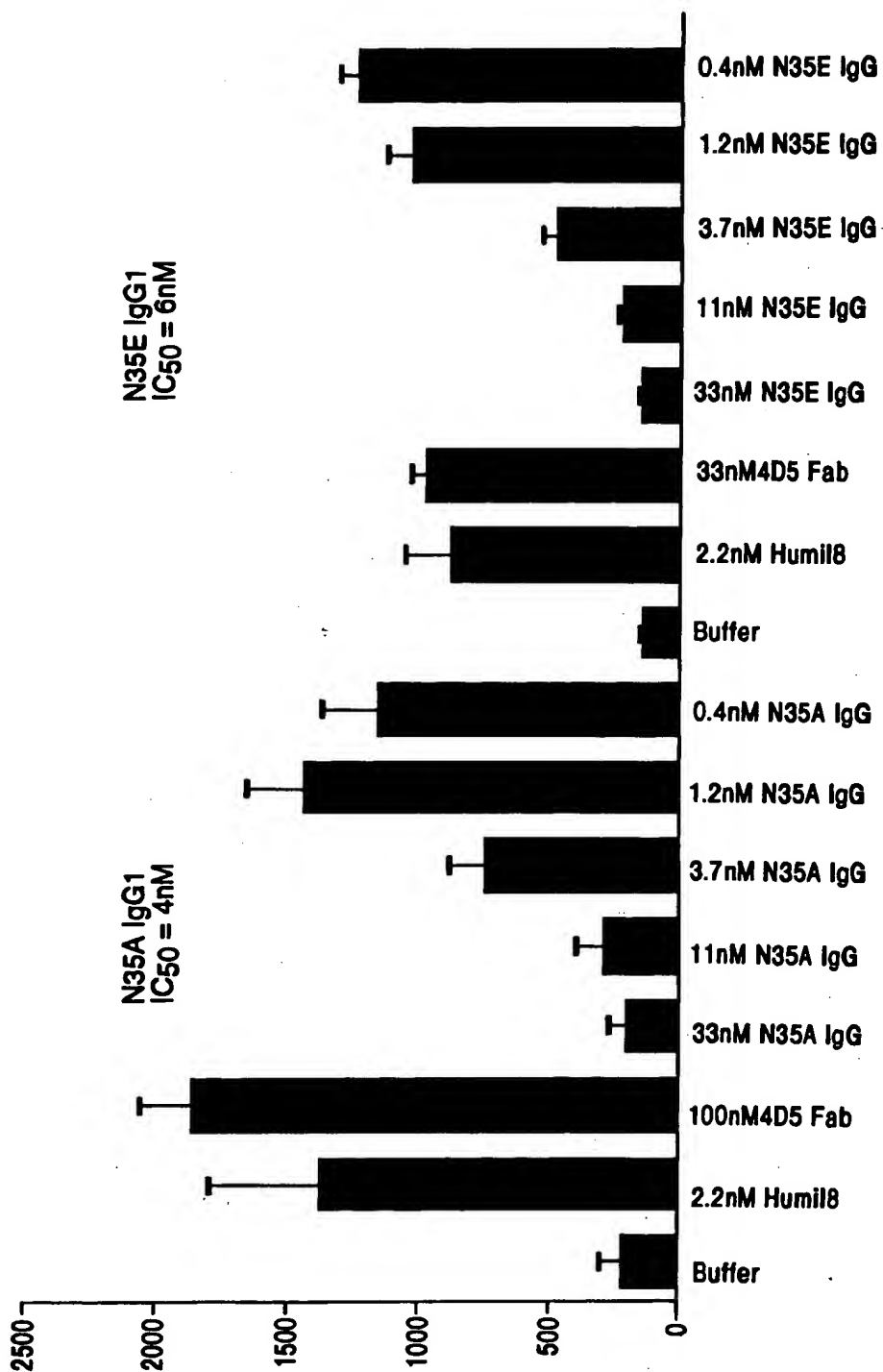


FIG. 50A

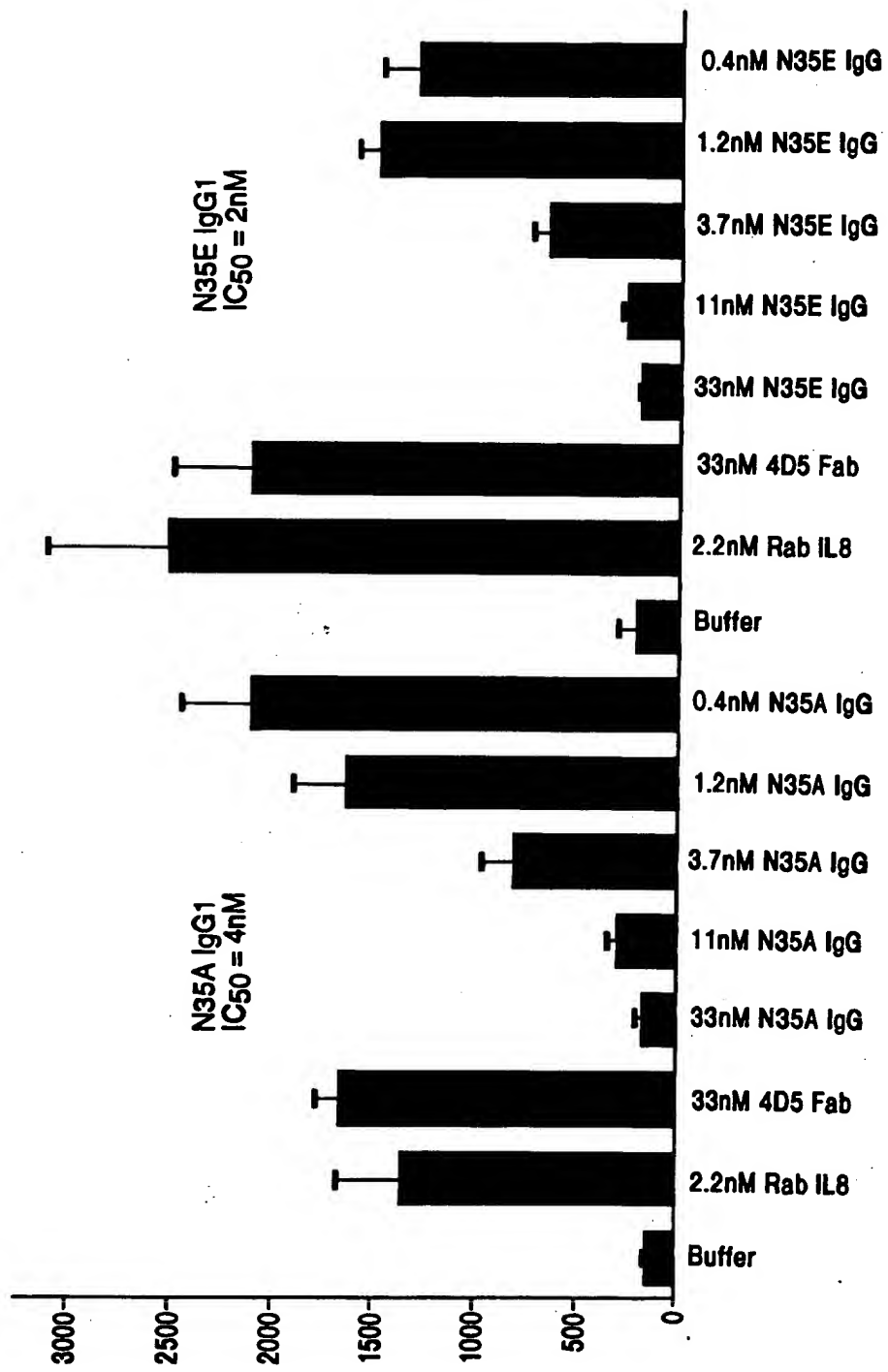
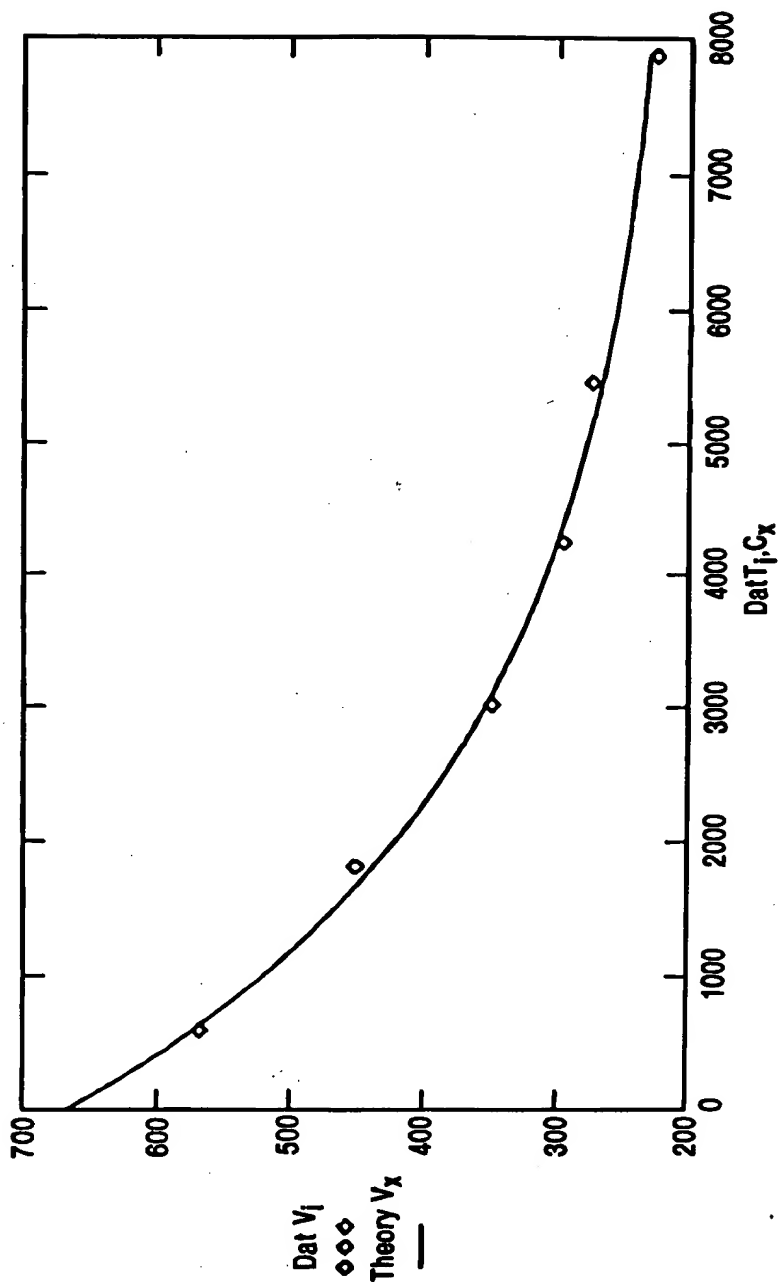


FIG. 50B



Representative Conc versus Time Plot. Shown is the kinetic data for 6G4V11N35A.IgG1

SAMPLE	k_a	k_d	K_d
Murine 6G4.2.5 IgG2a	8.3×10^5	2.9×10^{-4}	350pM
6G4V11N35A-IgG1	8.7×10^5	7.7×10^{-5}	88pM
6G4V11N35E-IgG1	3.0×10^6	1.4×10^{-4}	49pM

FIG. 51

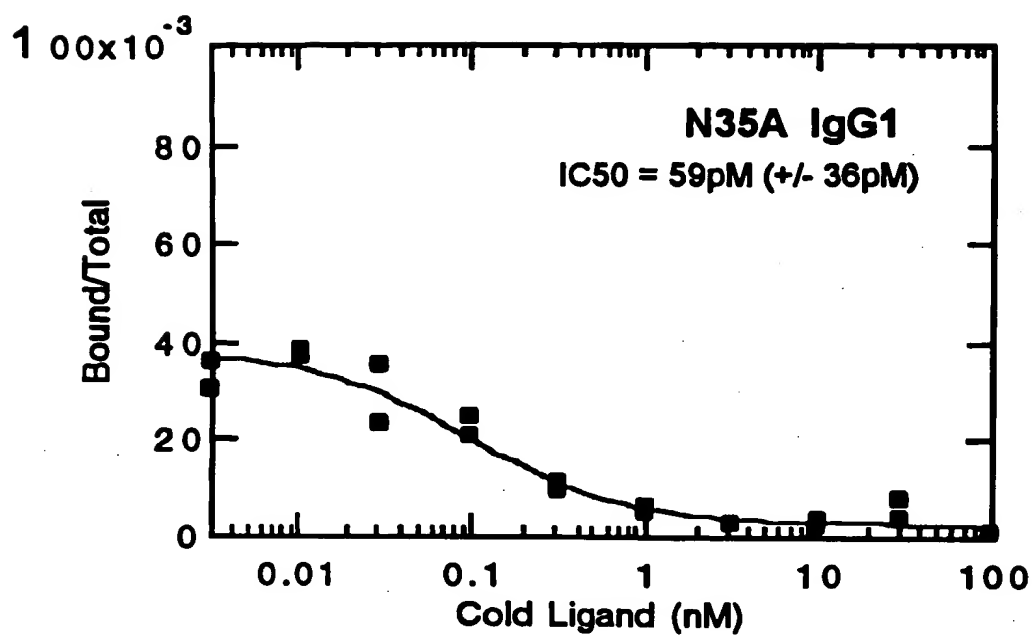


FIG. 52A

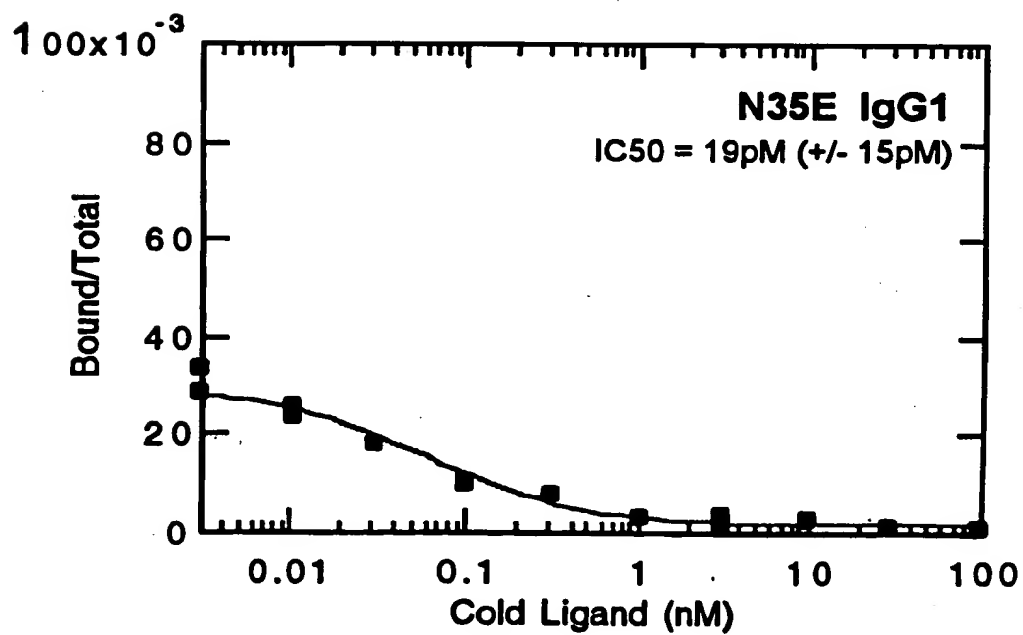


FIG. 52B



781 AAAAGGGTAT CTAGAGGTG AGGTGATTTT ATGAAAAAGA ATATCGCATT TCTTCCTTGCA
TTTTCCCATA GATCTCCAAC TCCACTAAAA TACTTTTCT TATAGCGTAA AGAAGAACGT
-1 M K K N I A F L L A

841 TCTATGTTTCG TTTTTTCTAT TGCTACAAAC GCGTACGCTG AGGTTTCAGCT AGTGCAGTCT
AGATACAAGC AAAAAAGATA ACGATGTTTG CGCATGCGAC TCCAAGTCGA TCACGTCAGA
-11 S M F V F S I A T N A Y A E V Q L V Q S

901 GGCGGTGGCC TGGTGCAGCC AGGGGGCTCA CTCCGTTTGT CCTGTGCAGC TTCTGGCTAC
CCGCCACCGG ACCACGTCGG TCCCCCGAGT GAGGCAAACA GGACACGTCG AAGACCGATG
8 G G G L V Q P G G S L R L S C A A S G Y

961 TCCTTCTCGA GTCACTATAT GCACTGGGTC CGTCAGGCCC CGGGTAAGGG CCTGGAATGG
AGGAAGAGCT CAGTGATATA CGTGACCCAG GCAGTCCGGG GCCCATTCCC GGACCTTACC
28 S F S S H Y M H W V R Q A P G K G L E W

1021 GTTGGATATA TTGATCCTTC CAATGGTGAA ACTACGTATA ATCAAAAGTT CAAGGGCCGT
CAACCTATAT AACTAGGAAG GTTACCACTT TGATGCATAT TAGTTTTCAA GTTCCCAGCA
48 V G Y I D P S N G E T T Y N O K F K G R

1081 TTCACTTTAT CTCGCGACAA CTCCAAAAAC ACAGCATACC TGCAGATGAA CAGCCTGCGT
AAGTGAAATA GAGCGCTGTT GAGGTTTTTG TGTCGTATGG ACGTCTACTT GTCGGACGCA
68 F T L S R D N S K N T A Y L Q M N S L R

1141 GCTGAGGACA CTGCCGTCTA TTA CTGTGCA AGAGGGGATT ATCGCTACAA TGGTGA CTGG
CGACTCCTGT GACGGCAGAT AATGACACGT TCTCCCCTAA TAGCGATGTT ACCACTGACC
88 A E D T A V Y Y C A R G D Y R Y N G D W

1201 TTCTTCGACG TCTGGGGTCA AGGAACCCTG GTCACCGTCT CCTCGGCCTC CACCAAGGGC
AAGAAGCTGC AGACCCCACT TCCCTGGGAC CAGTGGCAGA GGAGCCGGAG GTGGTTCCCG
108 F F D V W G Q G T L V T V S S A S T K G

1261 CCATCGGTCT TCCCCCTGGC ACCCTCCTCC AAGAGCACCT CTGGGGGCAC AGCGGCCCTG
GGTAGCCAGA AGGGGGACCG TGGGAGGAGG TTCTCGTGGA GACCCCGCTG TCGCCGGGAC
128 P S V F P L A P S S K S T S G G T A A L

1321 GGCTGCCTGG TCAAGGACTA CTTCCCCGAA CCGGTGACGG TGTCGTGGAA CTCAGGCGCC
CCGACGGACC AGTTCTTGAT GAAGGGGCTT GGCCACTGCC ACAGCACCTT GAGTCCGCGG
148 G C L V K D Y F P E P V T V S W N S G A

1381 CTGACCAGCG GCGTGCACAC CTTCCCGGCT GTCCTACAGT CCTCAGGACT CTA CTCCCTC
GACTGGTGC CACACGTGTG GAAGGGCCGA CAGGATGTCA GGAGTCTGA GATGAGGGAG
168 L T S G V H T F P A V L Q S S G L Y S L

1441 AGCAGCGTGG TGACCGTGCC CTCCAGCAGC TTGGGCACCC AGACCTACAT CTGCAACGTG
TCGTGCGACC ACTGGCACGG GAGGTCGTG AACCCTGGG TCTGGATGTA GACGTTGCAC
188 S S V V T V P S S S L G T Q T Y I C N V

1501 AATCACAAGC CCAGCAACAC CAAGGTGAC AAGAAAGTTG AGCCCAAATC TTGTGACAAA
TTAGTGTTTC GGTGCTGTG GTTCCAGCTG TTCTTTCAAC TCGGGTTTAG AACACTGTTT
208 N H K P S N T K V D K K V E P K S C D K

1561 ACTCACACAT GCCCGCCGTGA
TGAGTGTGTA CGGGCGGCACT
228 T H T C P P O

FIG. 53

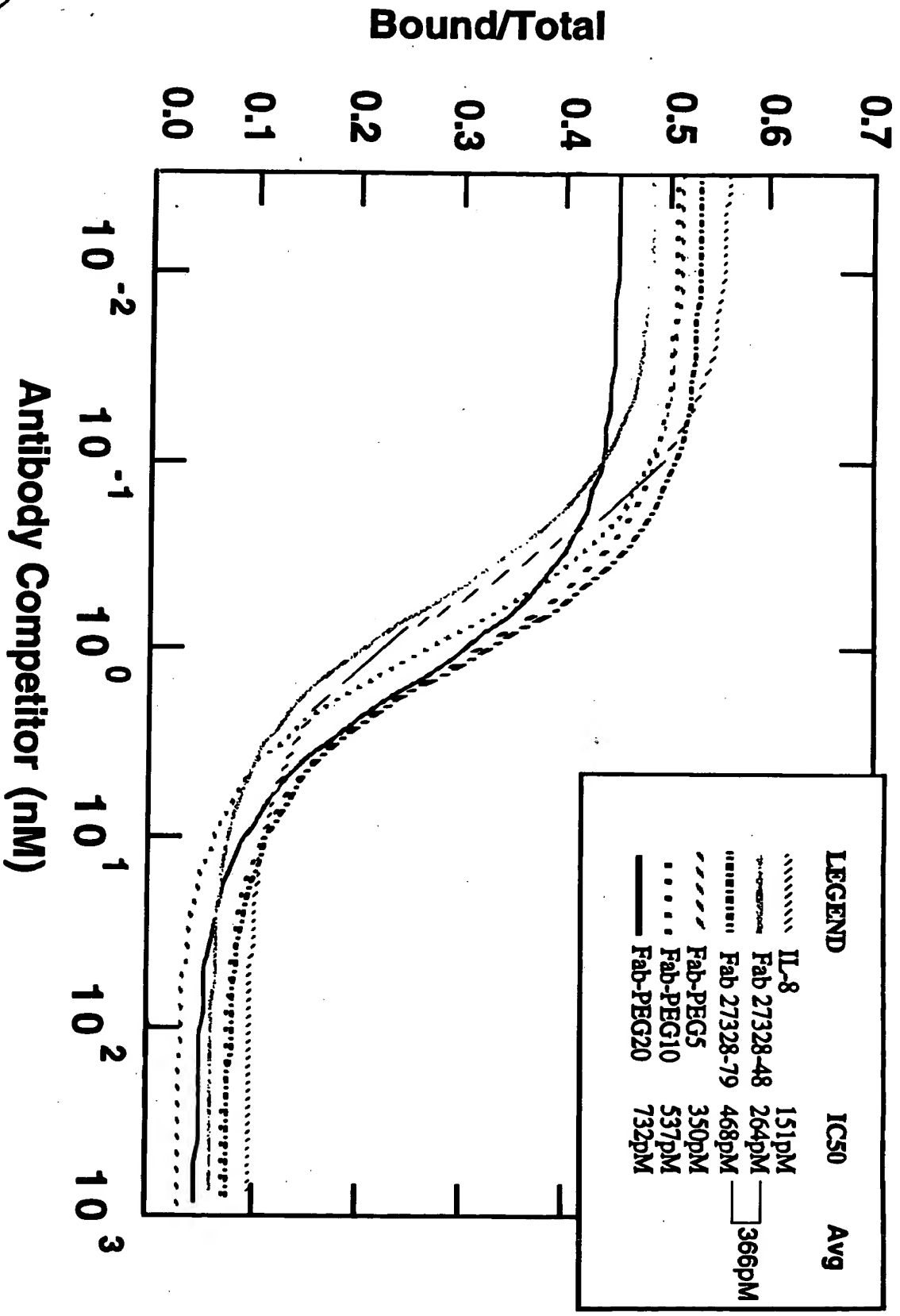
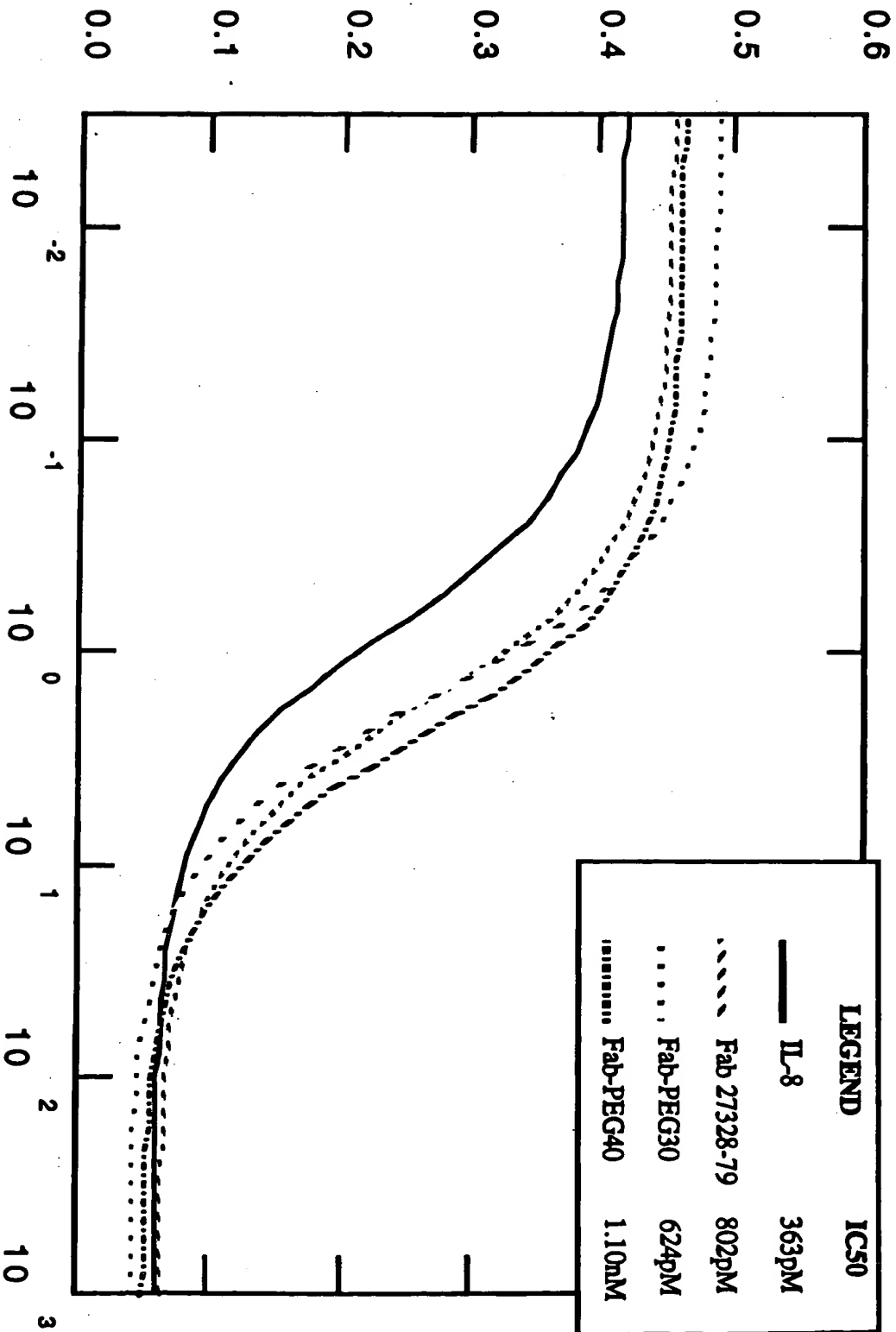


FIG. 54A



Bound/Total



Antibody Competitor (nM)

FIG. 54B

LEGEND		IC50
—	IL-8	363pM
- - -	Fab 27328-79	802pM
.....	Fab-PEG30	624pM
	Fab-PEG40	1.10nM

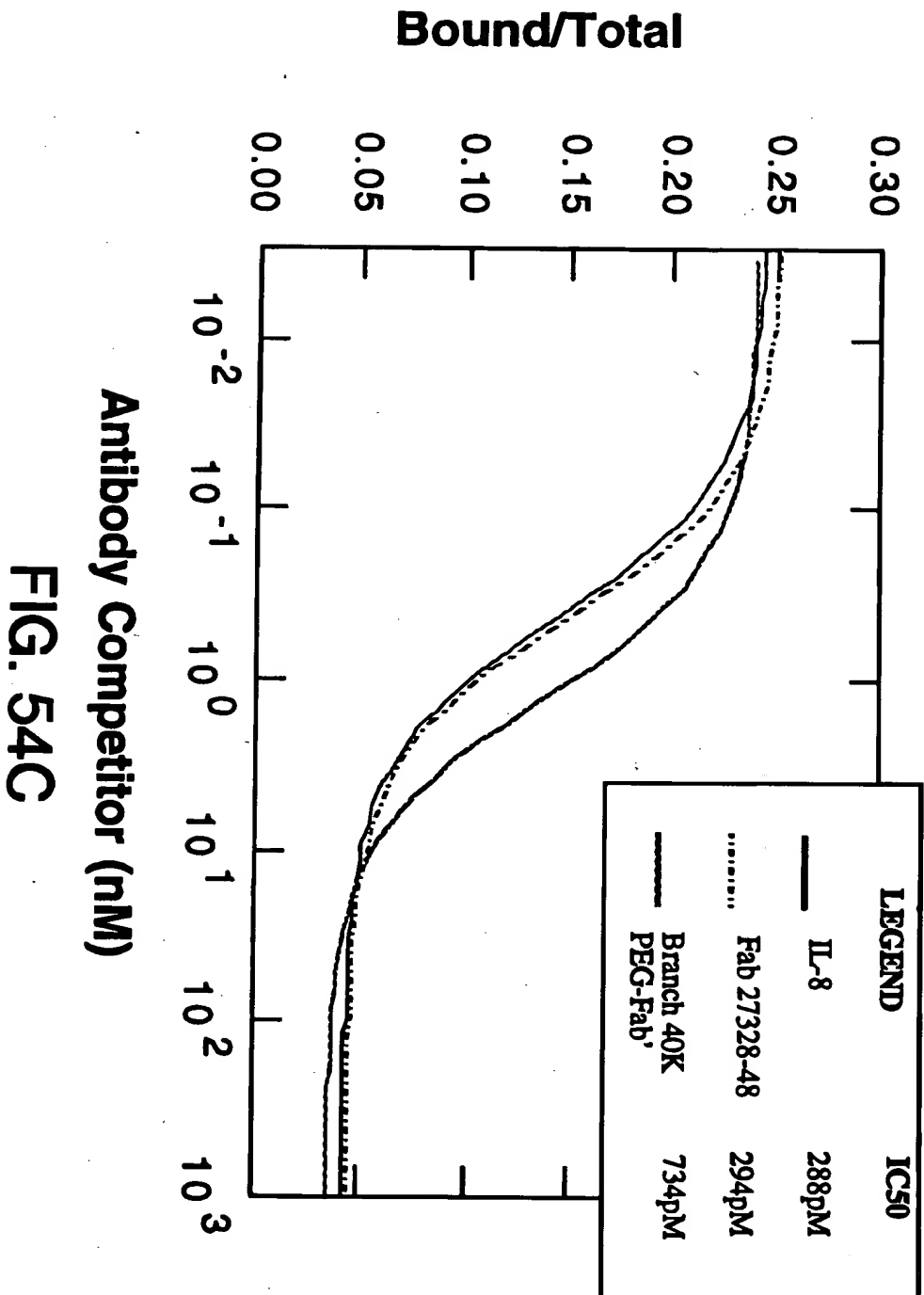


FIG. 54C

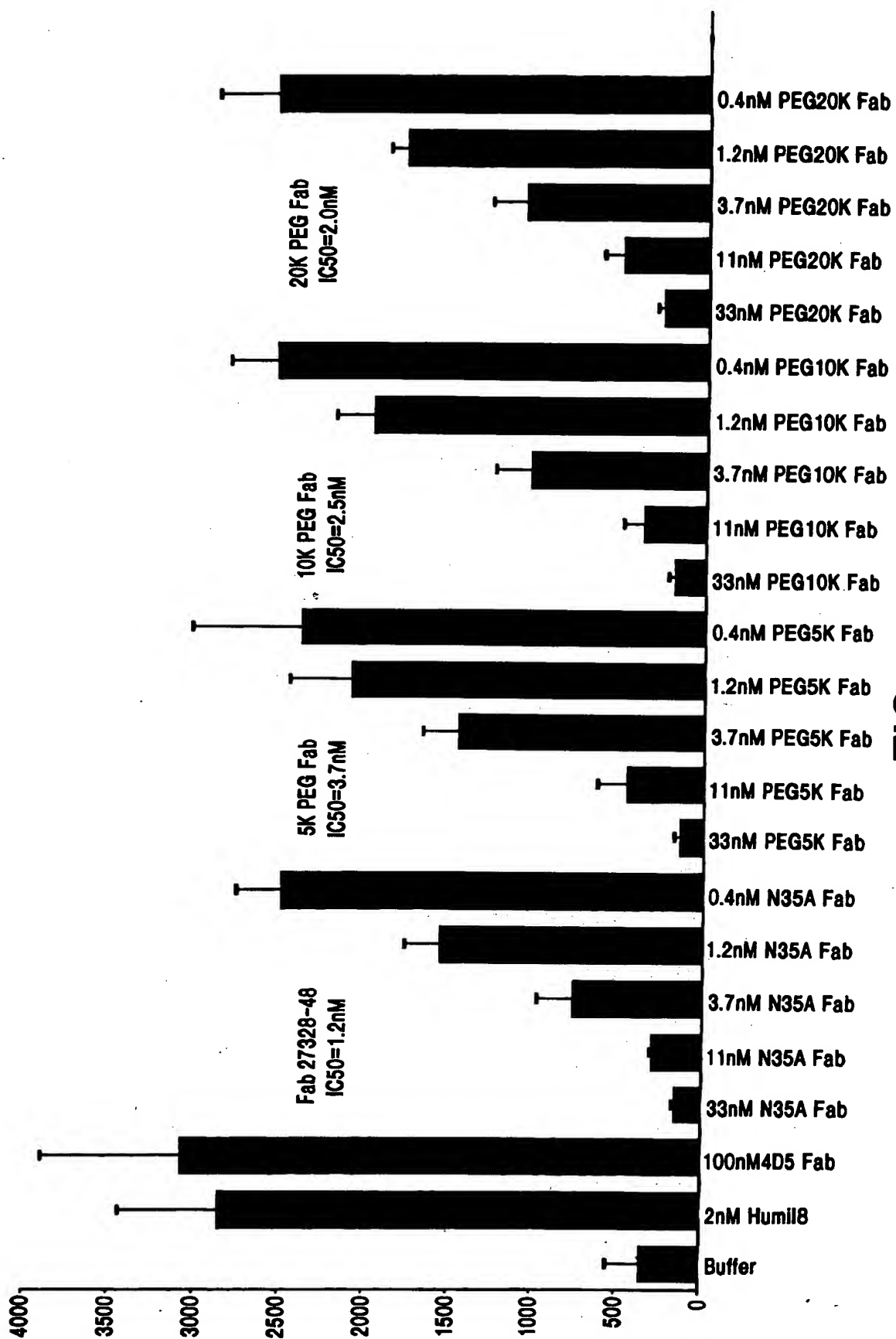


FIG. 55A

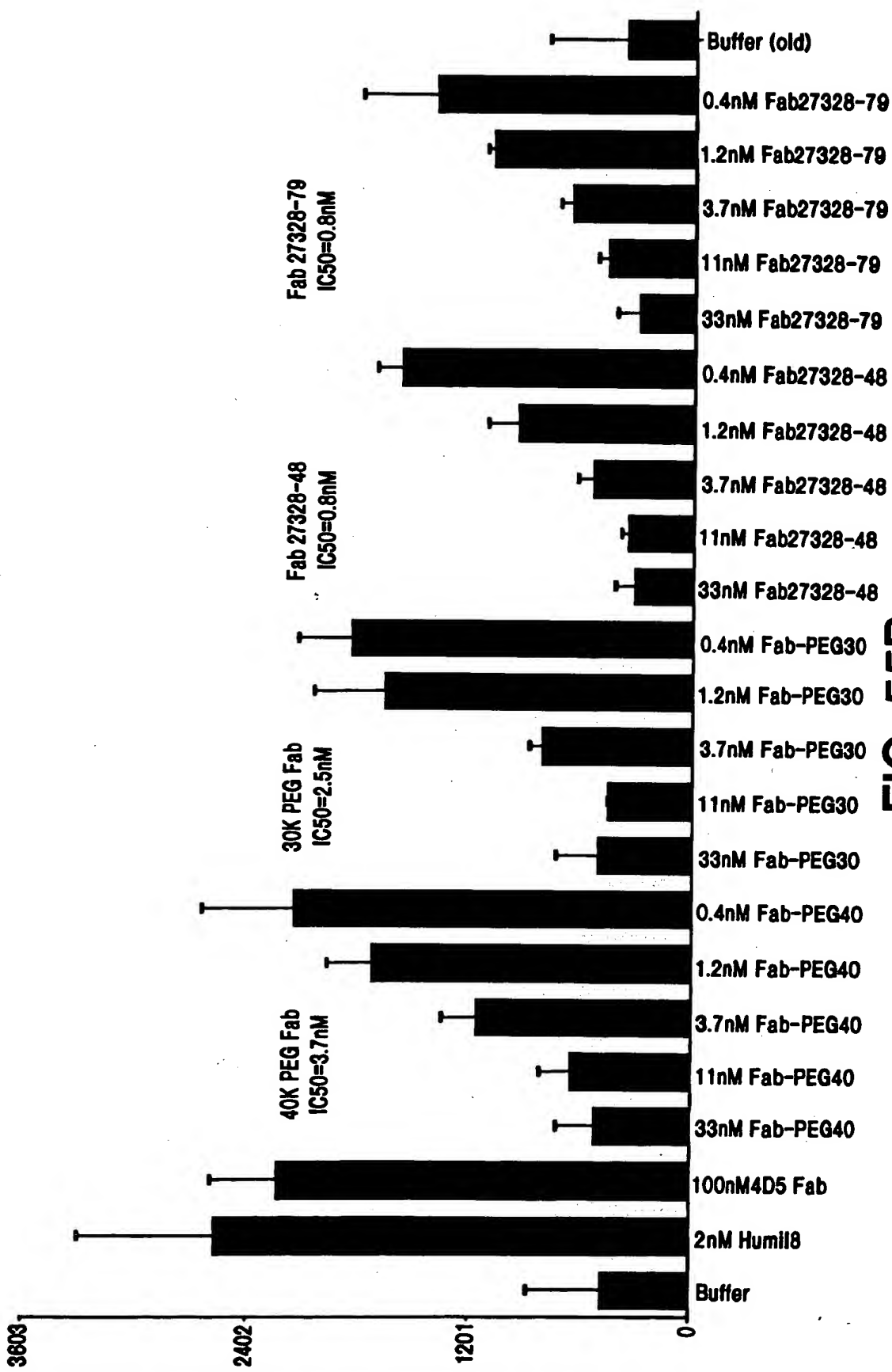


FIG. 55B

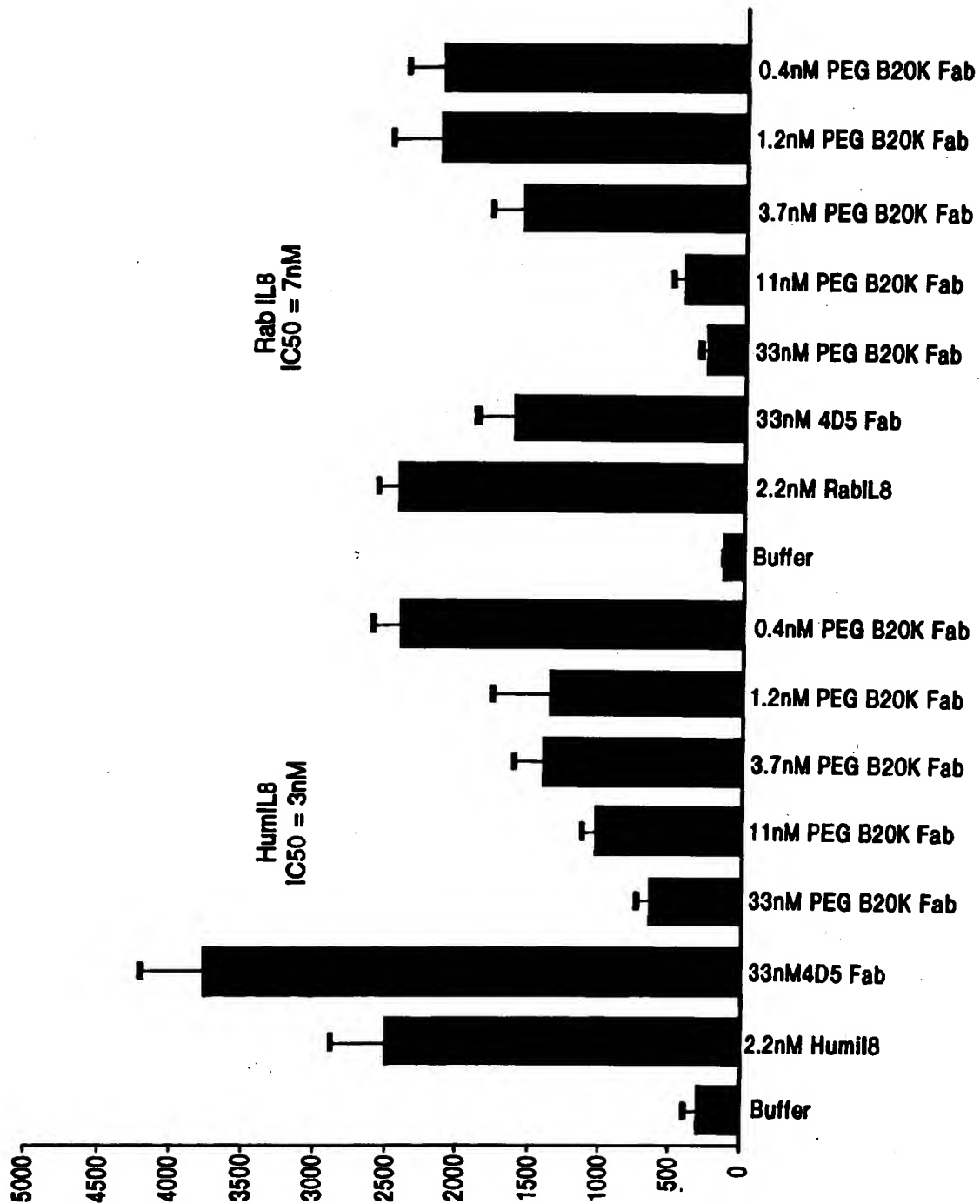
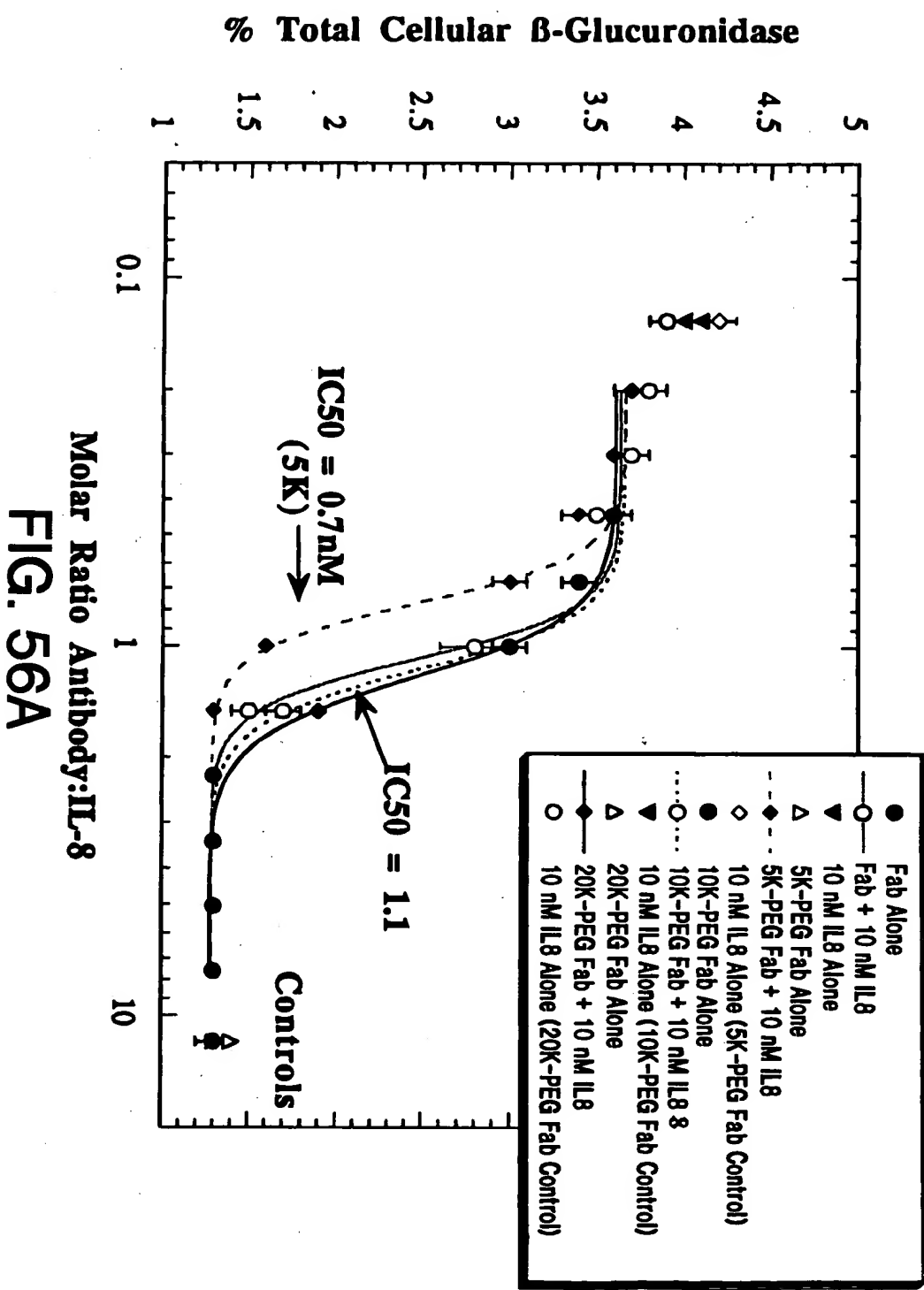
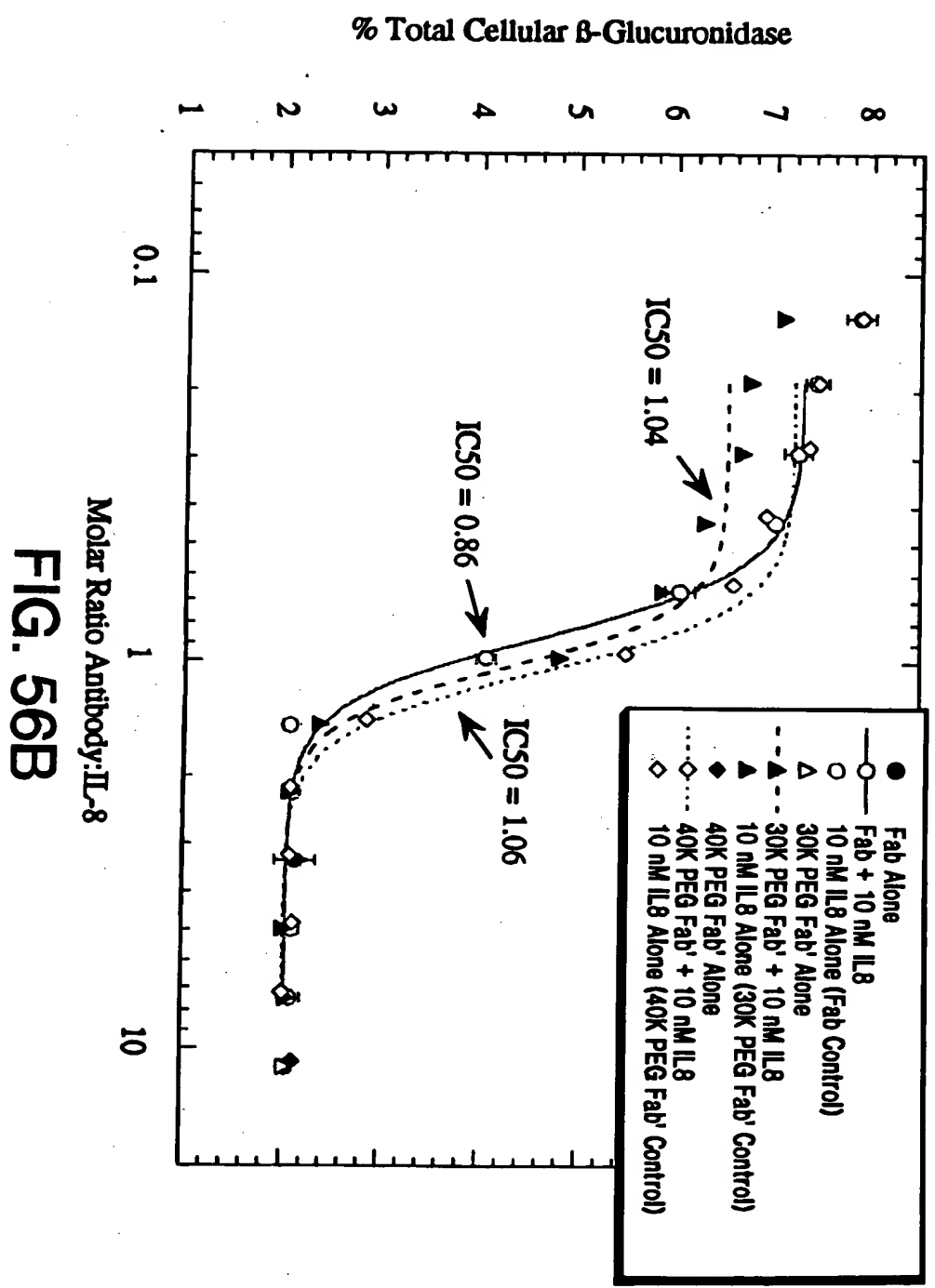


FIG. 55C





% Total Cellular β -Glucuronidase Activity

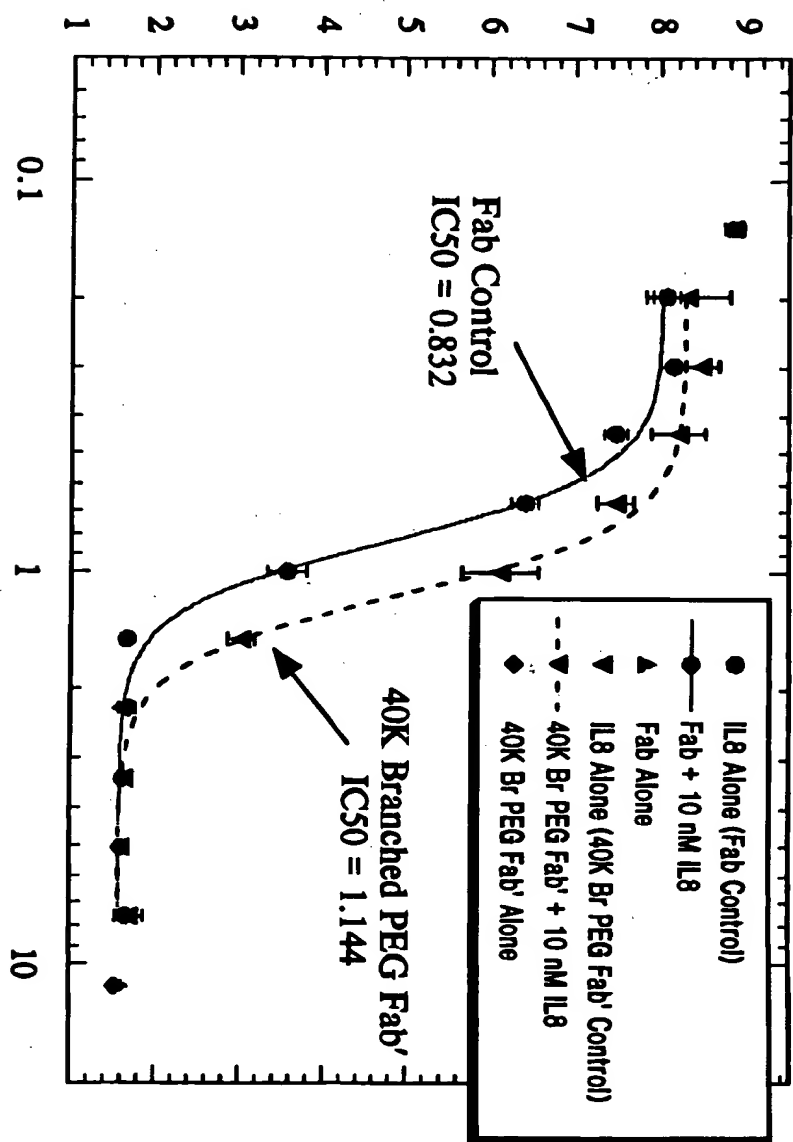
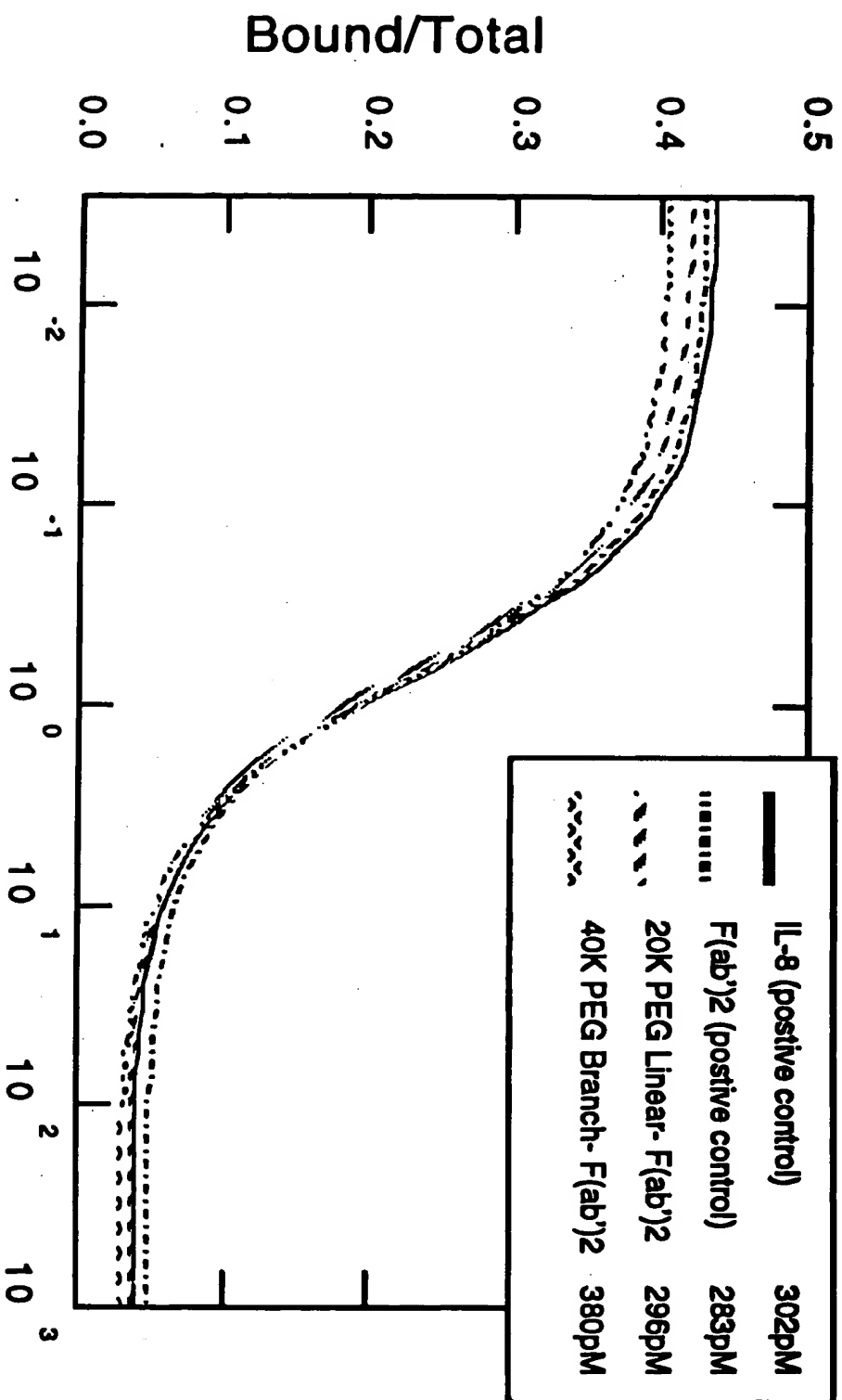
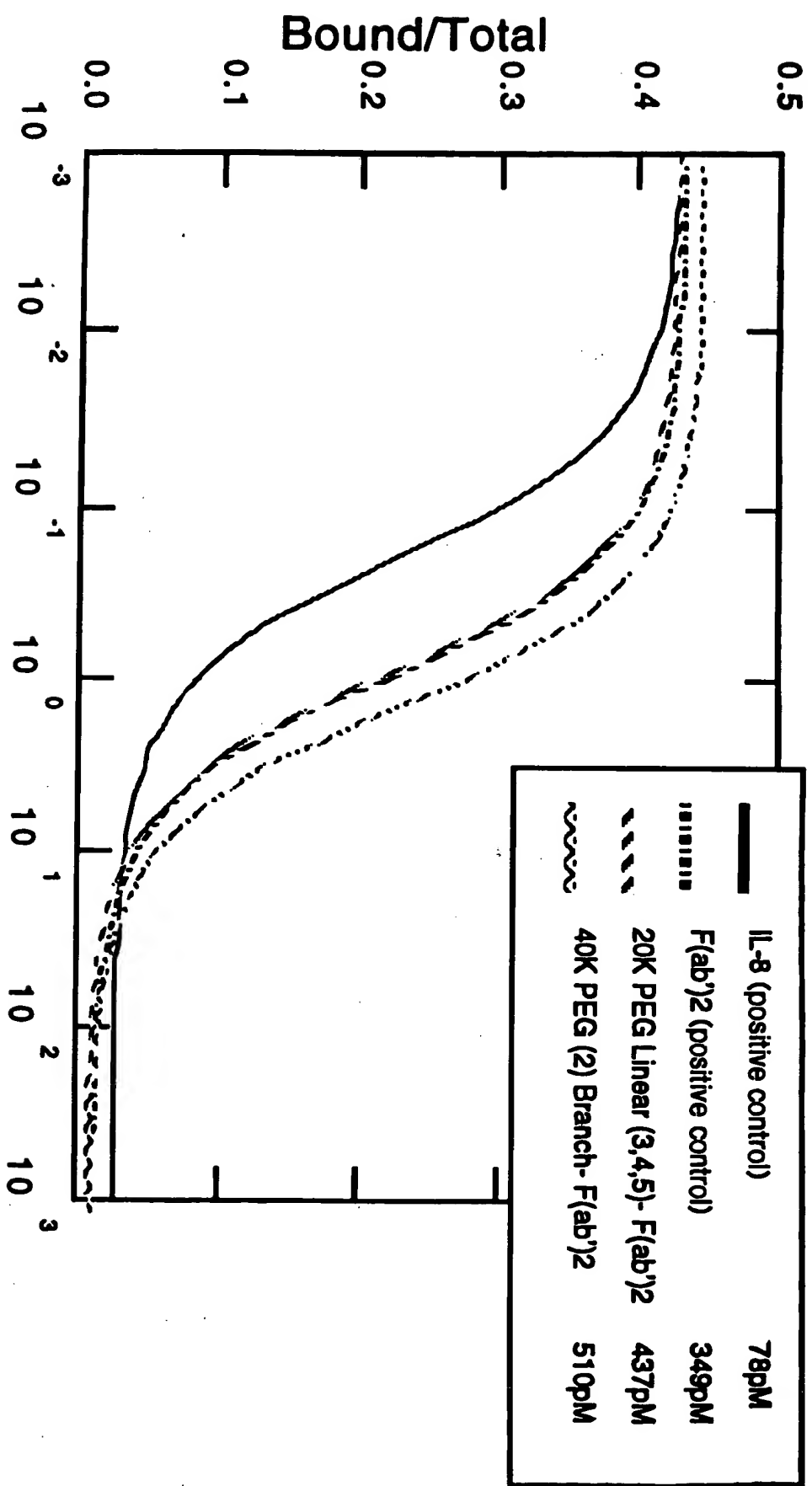


FIG. 56C



Pegylated F(ab')₂ (nM)
FIG. 57A



Pegylated F(ab')₂ (nM)
FIG. 57B

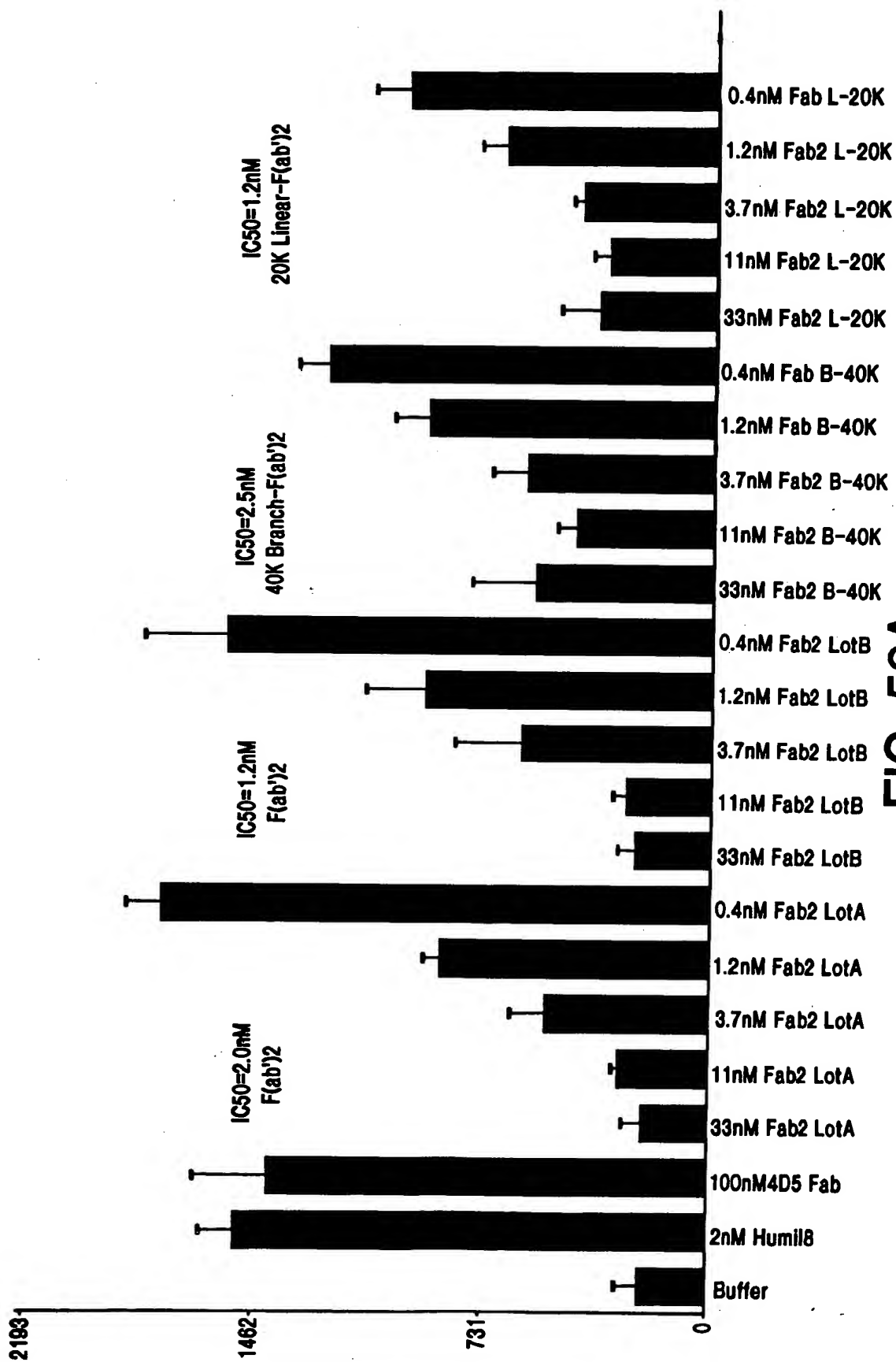


FIG. 58A

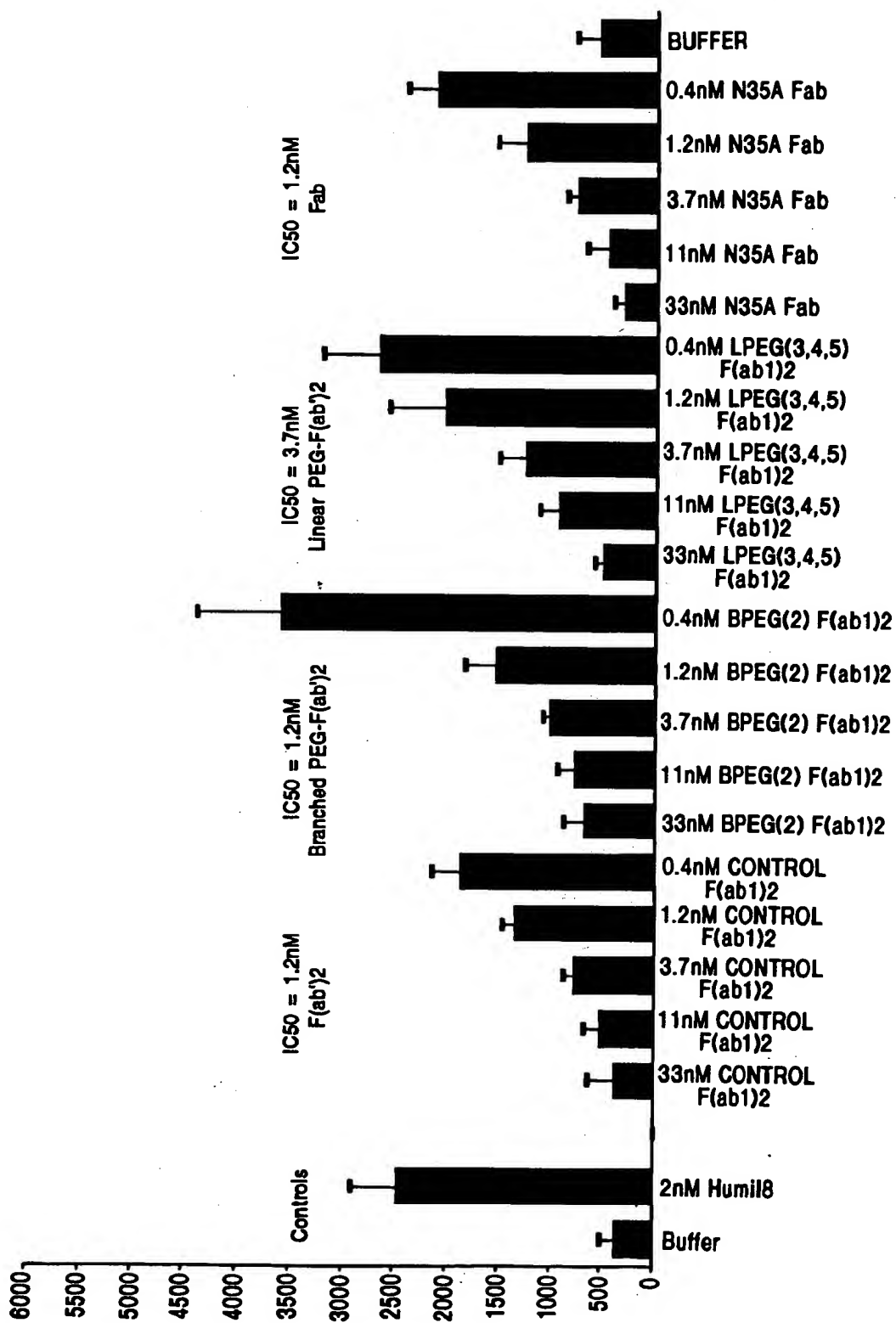
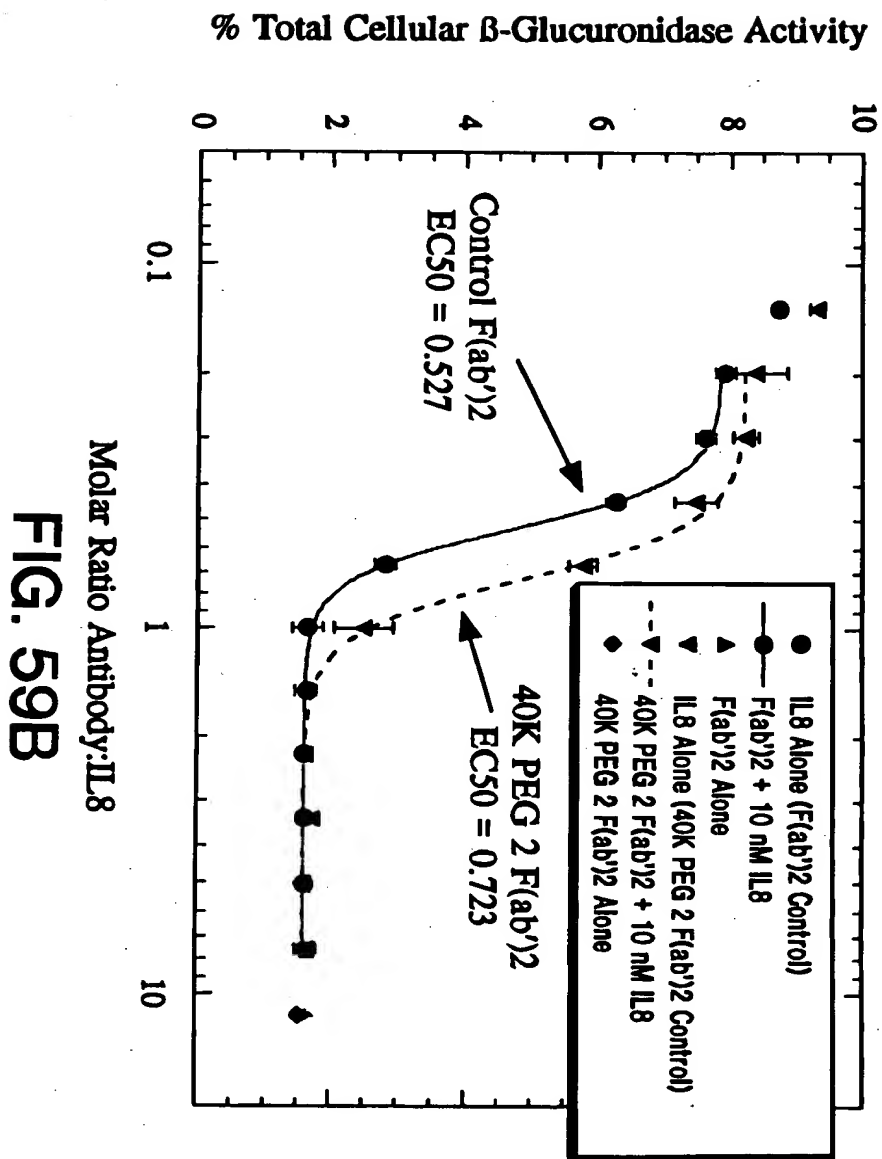
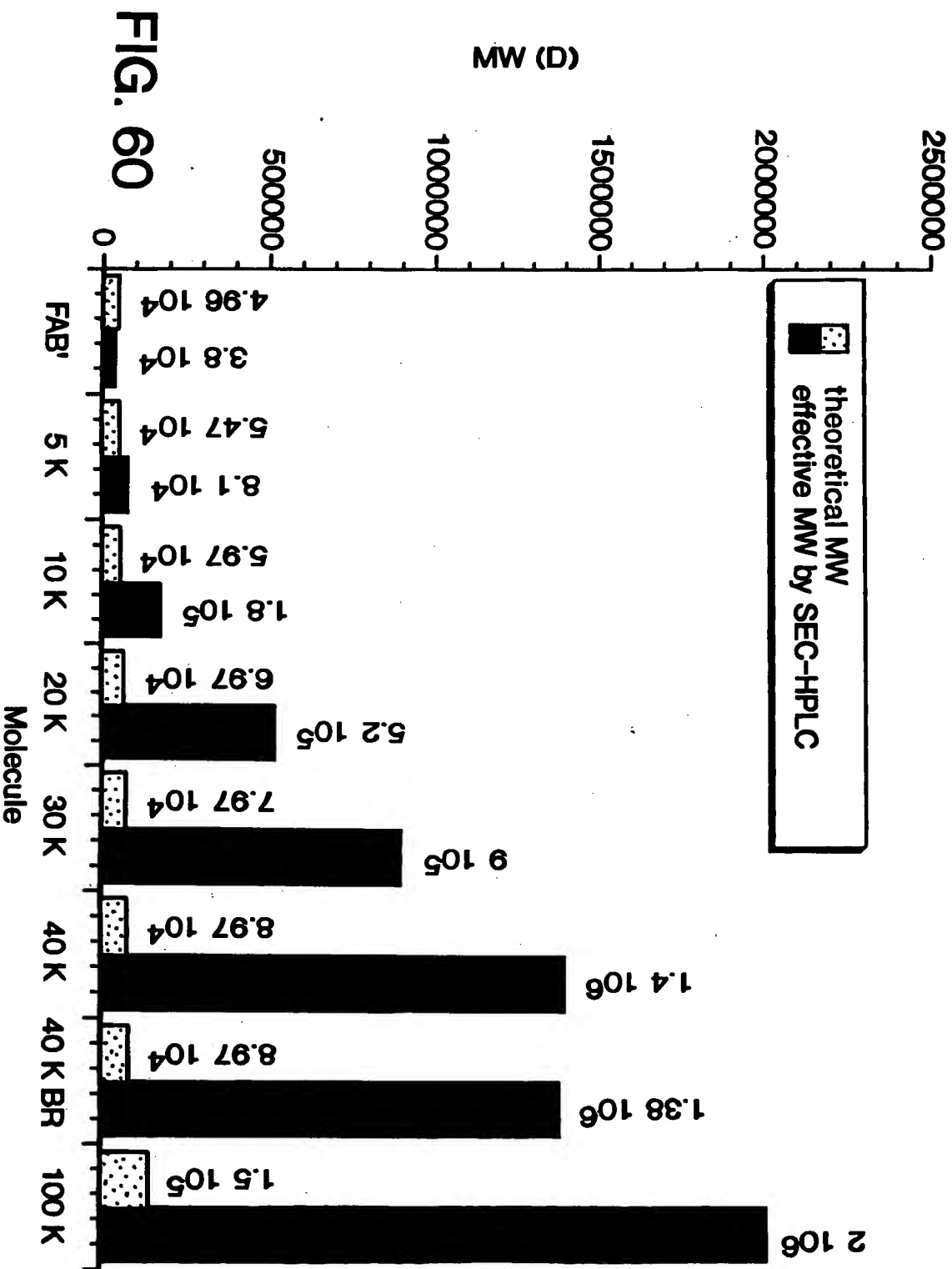
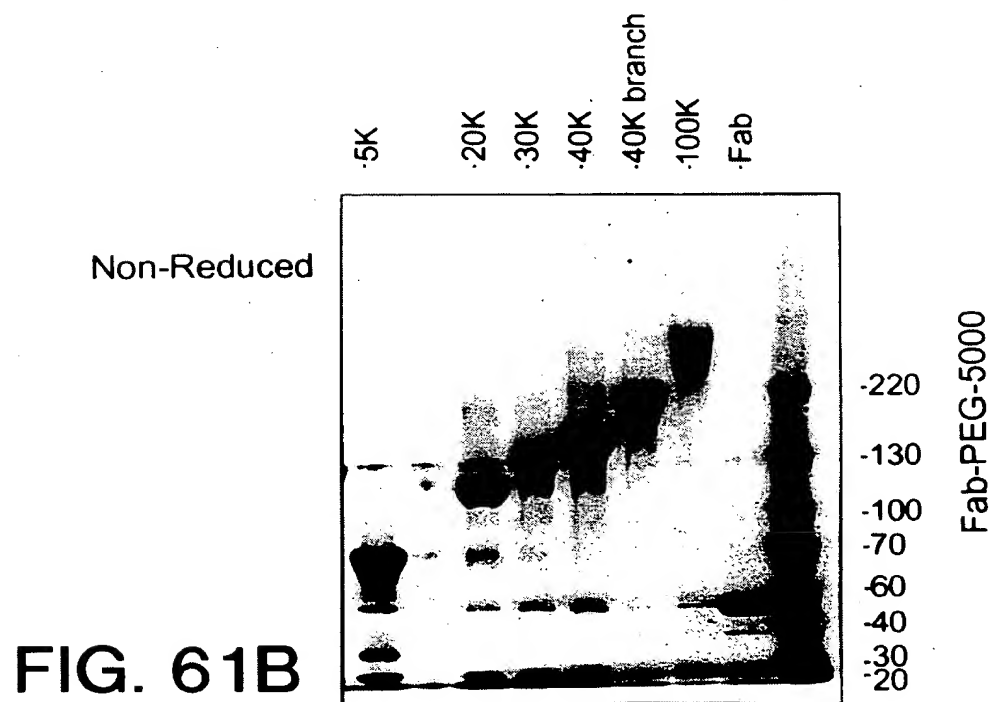
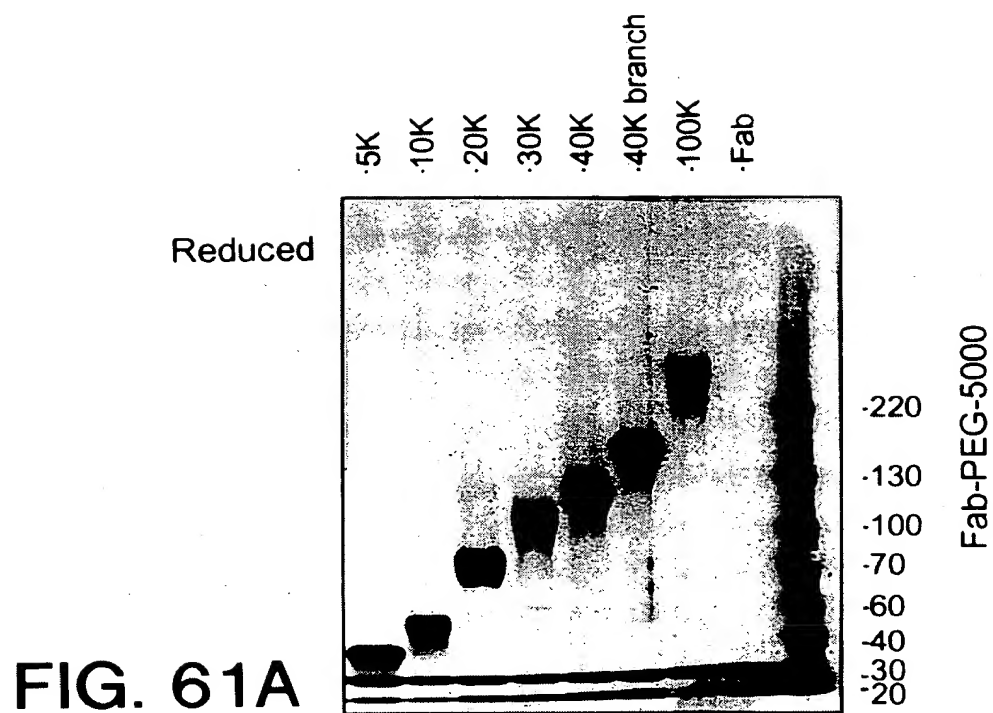


FIG. 58B







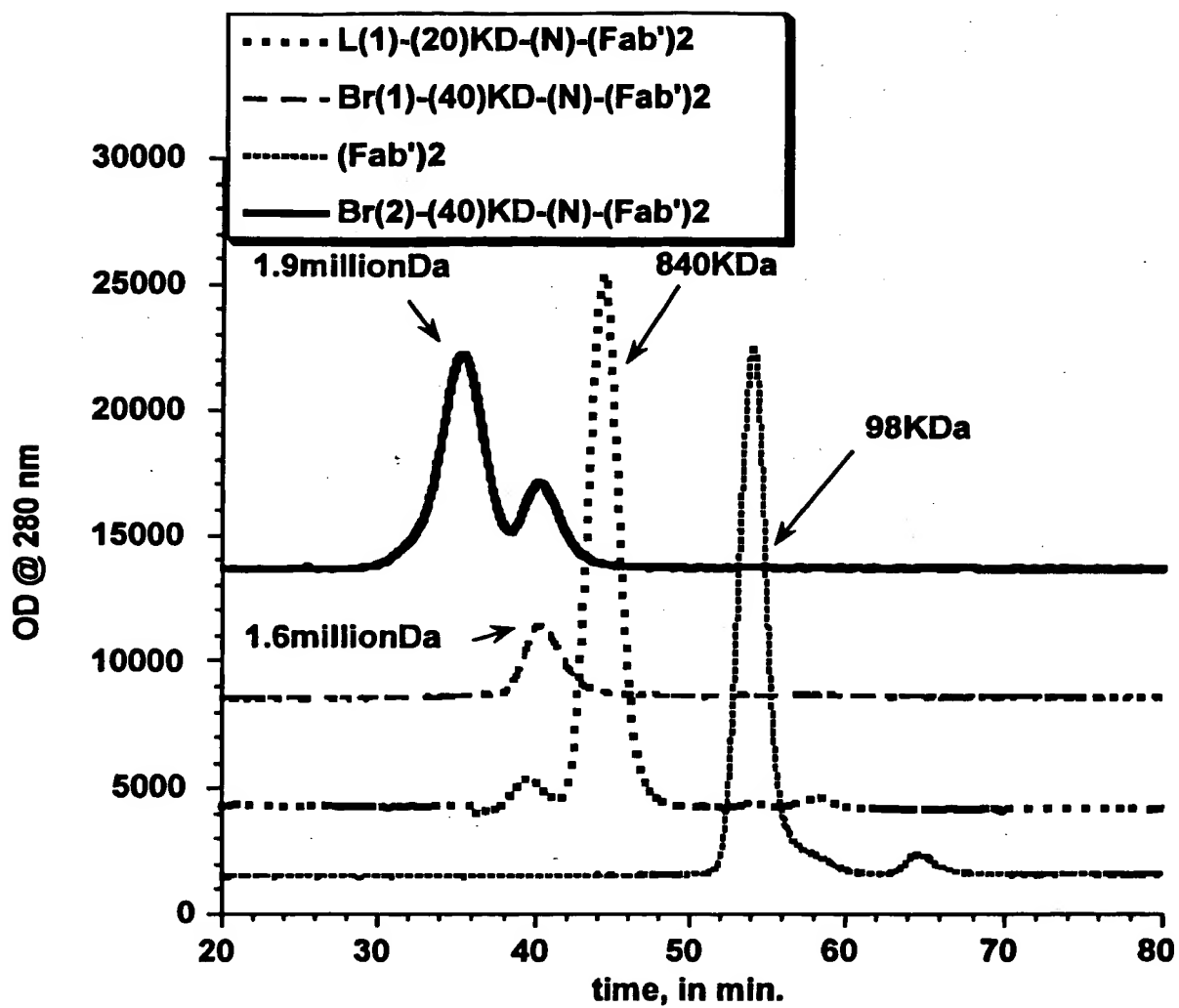


FIG. 62

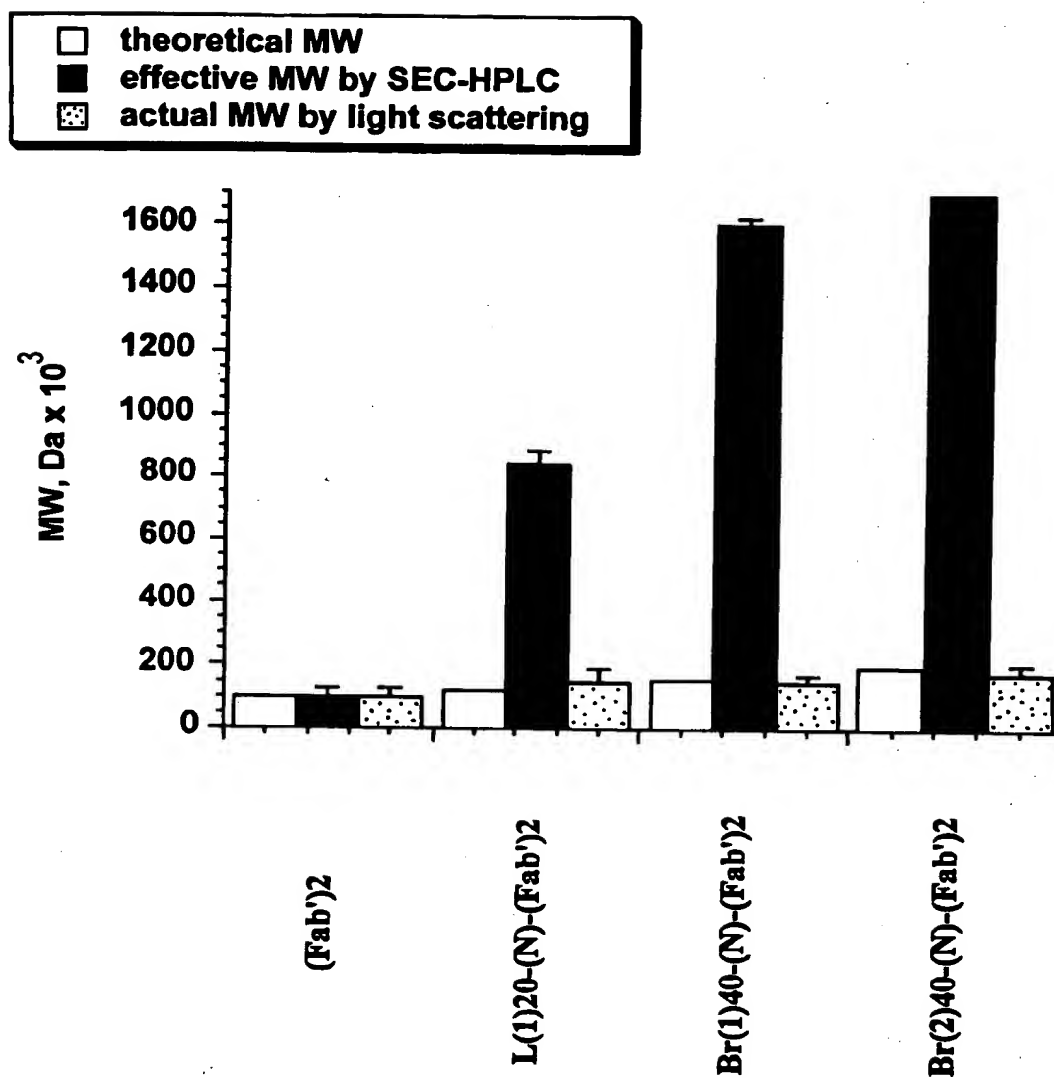


FIG. 63

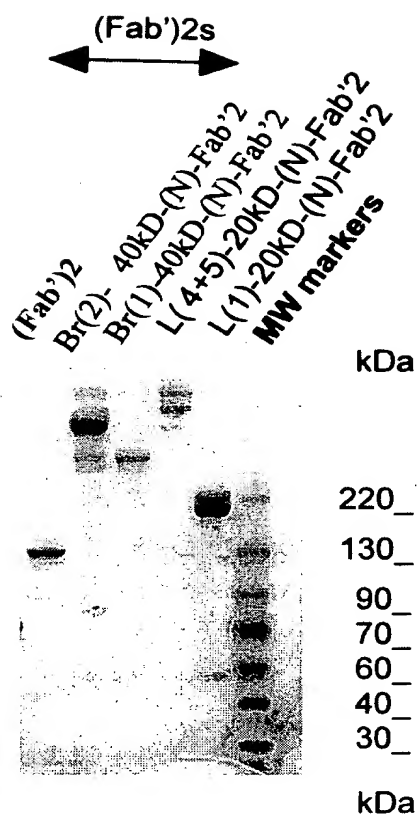
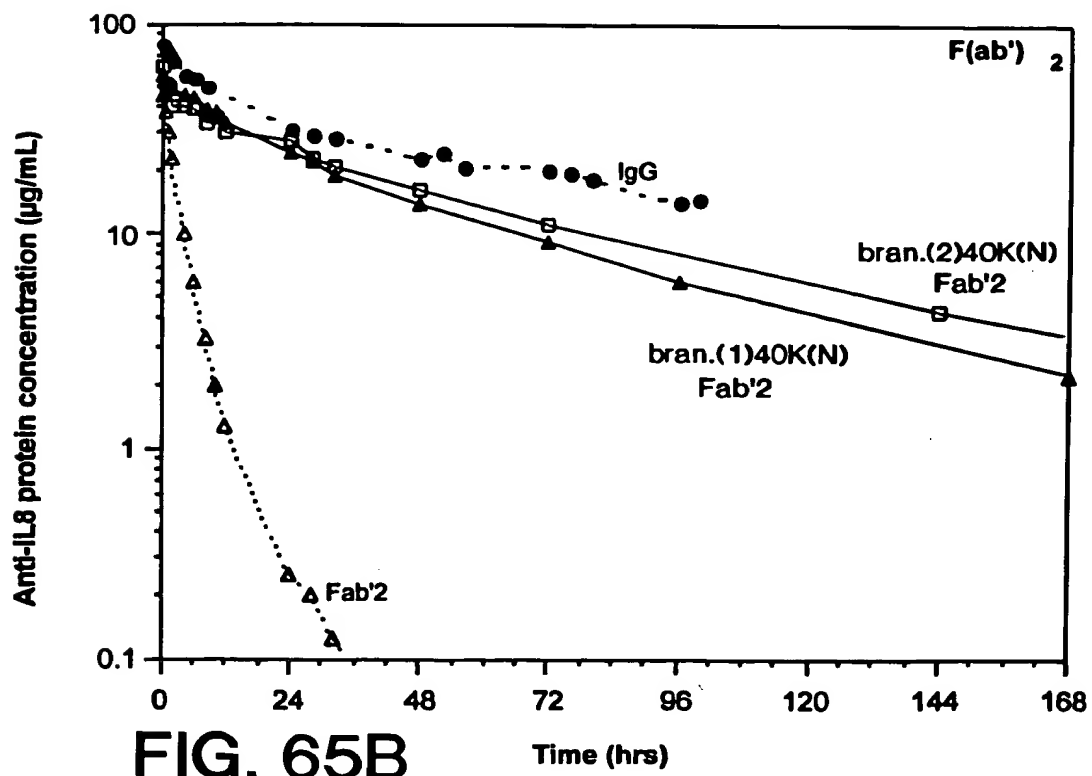
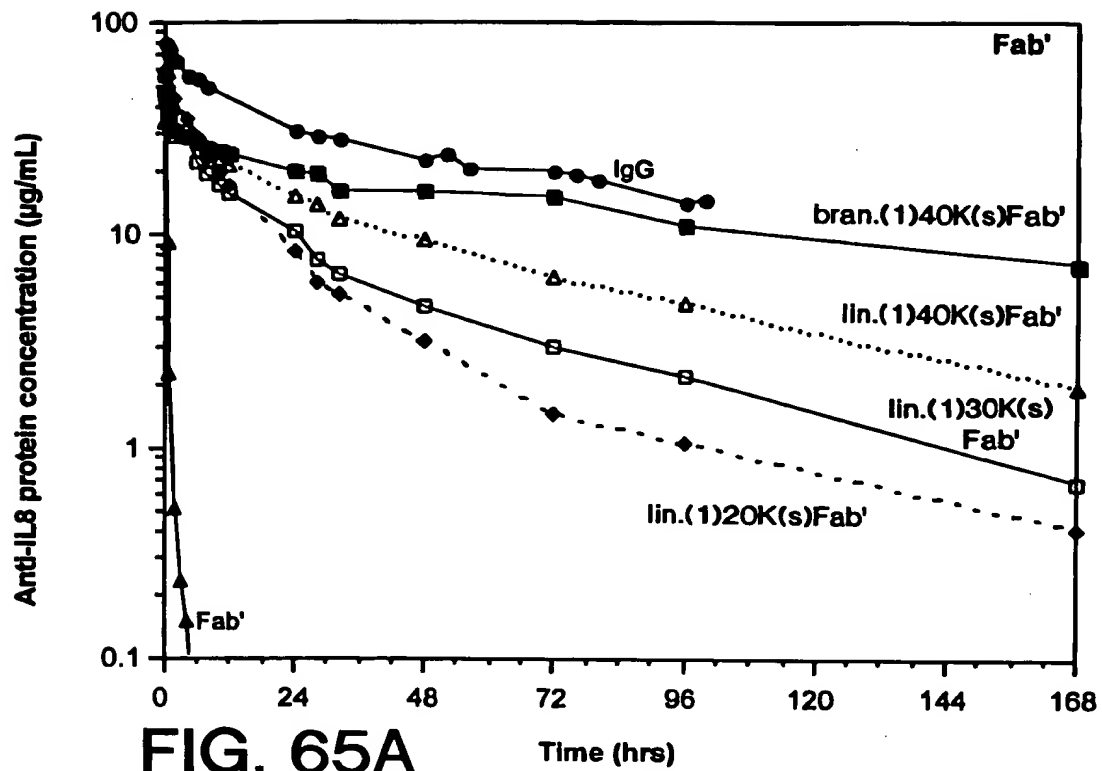


FIG. 64



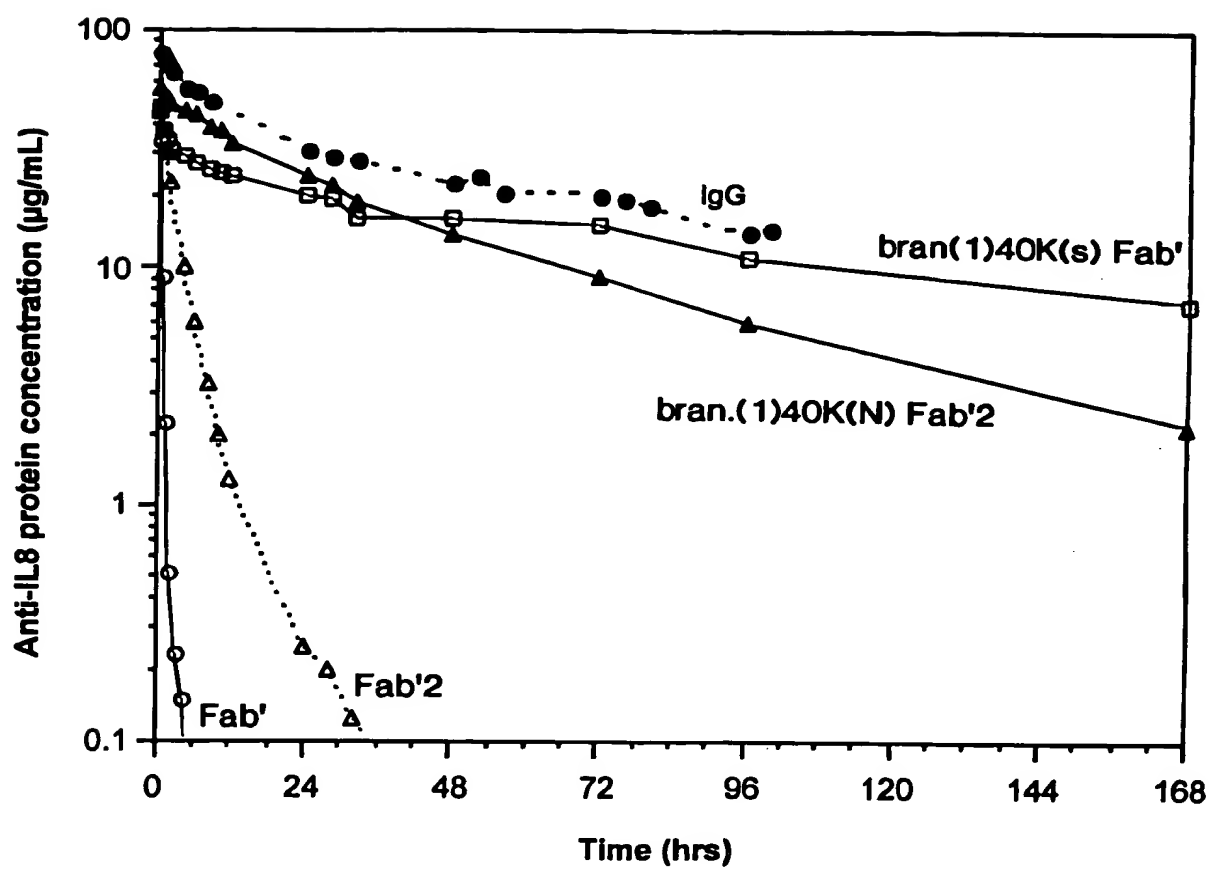


FIG. 66

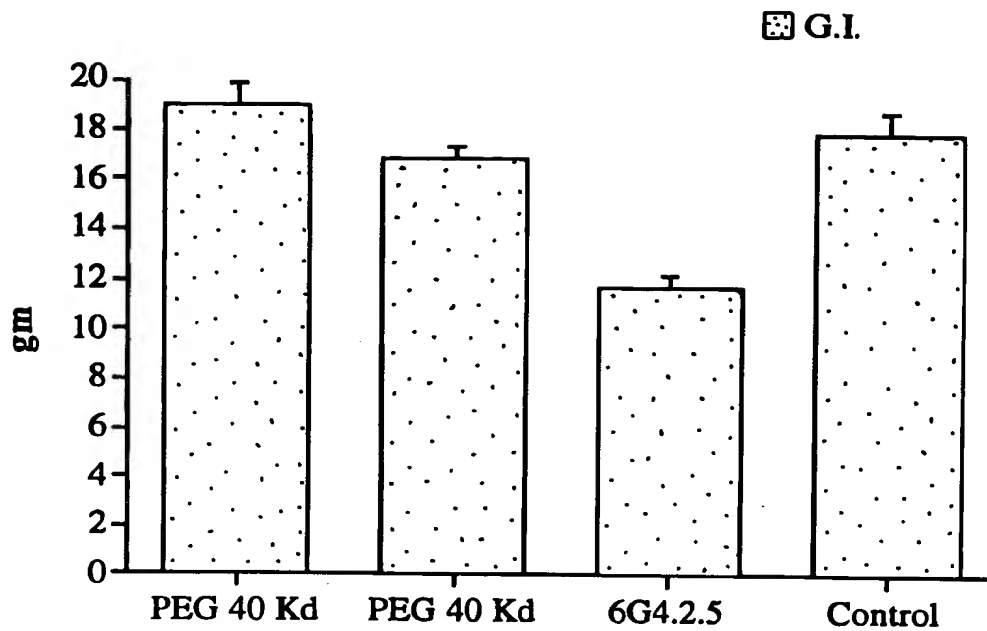


FIG. 67

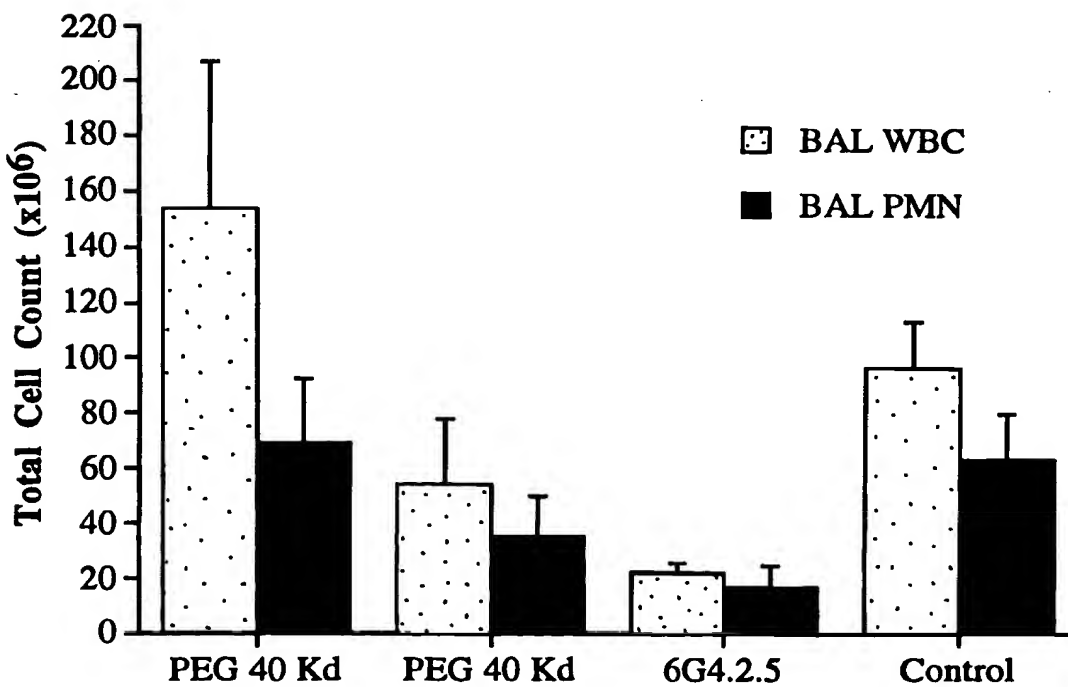


FIG. 68

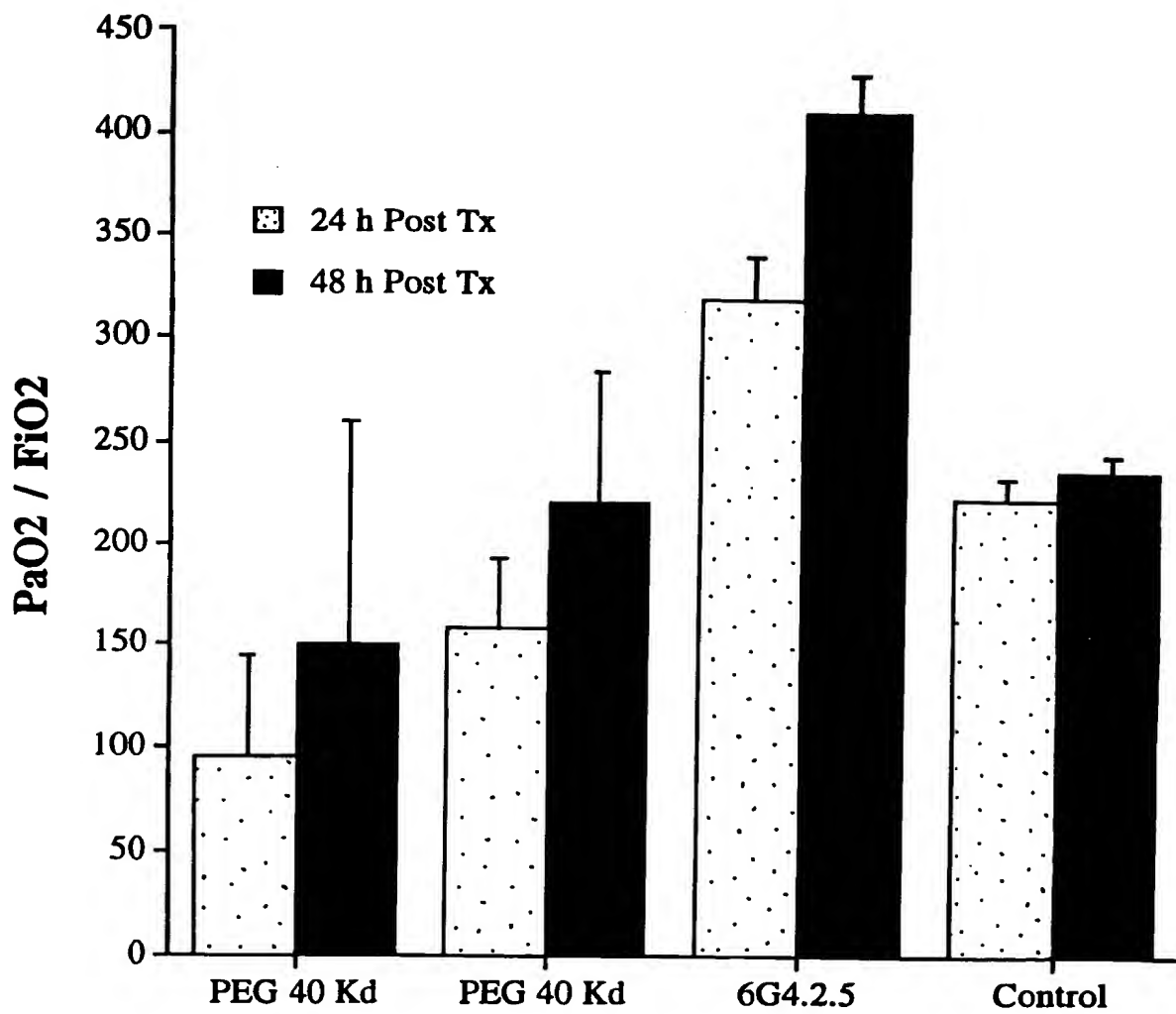


FIG. 69